

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 08:43:19 ; Search time 1609 Seconds
(without alignments)
3534.144 Million cell updates/sec
Title: US-09-925-139-3_COPY_1631_1769
Perfect score: 139
Sequence: 1 9gatggggttagcagaa.....ctatcctaaggccactgg 139
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 1010434
Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl:

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.em.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.or.*
- 21: em.ov.*
- 22: em.pat.*
- 23: em.ph.*
- 24: em.pl.*
- 25: em.ro.*
- 26: em.sts.*
- 27: em.un.*
- 28: em.vi.*
- 29: em.htg.hum.*
- 30: em.htg.inv.*
- 31: em.htg.other.*
- 32: em.htg.mus.*
- 33: em.htg.pln.*
- 34: em.htg.rod.*
- 35: em.htg.nam.*
- 36: em.htg.vrt.*
- 37: em.sv.*
- 38: em.htgo.hum.*
- 39: em.htgo.mus.*
- 40: em.htgo.other.*
- 41: em.htgo.mus.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	21	15.1	21	6	BD102270	BD102270 Method of
C 2	17.6	12.7	30	11	BX323474	BX323474 Arabidops
C 3	17.2	12.4	22	6	E25734	E25734 Method for
C 4	16.8	12.1	21	6	BD101979	BD101979 Novel G p
C 5	16.8	12.1	21	6	BD131270	BD131270 Novel G p
C 6	16.8	12.1	30	6	AR262363	AR262363 Sequence
C 7	16.2	11.7	22	6	AR129513	AR129513 Sequence
C 8	16.2	11.7	28	6	E24992	E24992 Apoptosis-i
C 9	16.2	11.7	29	6	AX597968	AX597968 Sequence
C 10	16.2	11.7	30	6	AR018179	AR018179 Sequence
C 11	16.2	11.7	30	6	AX180867	AX180867 Sequence
C 12	16	11.5	25	6	E28689	E28689 Primer for
C 13	16	11.2	26	6	A64642	A64642 Sequence 8
C 14	15.6	11.2	30	6	AR009754	AR009754 Sequence
C 15	15.6	11.2	30	6	E73485	E73485 Sequence 7
C 16	15.6	11.2	30	6	E81194	E81194 Sequence 7
C 17	15.4	11.1	25	6	AX081599	AX081599 Sequence
C 18	15.4	11.1	25	6	AX374780	AX374780 Sequence
C 19	15.4	11.1	29	6	BD169474	BD169474 Novel gua
C 20	15.2	10.9	20	6	AX323427	AX323427 Sequence
C 21	15.2	10.9	23	6	AR142933	AR142933 Sequence
C 22	15.2	10.9	30	6	AR277835	AR277835 Sequence
C 23	15.2	10.9	30	6	AR279994	AR279994 Sequence
C 24	15.2	10.9	30	6	BD128452	BD128452 Solid pha
C 25	15.2	10.9	30	6	BD133164	BD133164 Method of
C 26	15.2	10.9	30	6	I08474	I08474 Sequence 12
C 27	15	10.8	25	6	AR147819	AR147819 Sequence
C 28	15	10.8	25	6	AX534165	AX534165 Sequence
C 29	15	10.8	25	6	AX534166	AX534166 Sequence
C 30	15	10.8	25	6	AX534167	AX534167 Sequence
C 31	15	10.8	26	6	A62920	A62920 Sequence 16
C 32	15	10.8	26	6	I09030	I09030 Sequence 1
C 33	15	10.8	29	6	AR174575	AR174575 Sequence
C 34	15	10.8	29	6	AX280176	AX280176 Sequence
C 35	15	10.8	29	6	AX598144	AX598144 Sequence
C 36	15	10.8	30	6	I26957	I26957 Sequence 6
C 37	14.8	10.6	25	6	AX196921	AX196921 Sequence
C 38	14.8	10.6	27	6	BD133891	BD133891 Alkali ce
C 39	14.8	10.6	30	6	E07789	E07789 PCR primer
C 40	14.8	10.6	30	6	E07789	E07789 PCR primer
C 41	14.6	10.5	24	6	AX172298	AX172298 Sequence
C 42	14.6	10.5	24	6	AX291985	AX291985 Sequence
C 43	14.6	10.5	24	6	AX300811	AX300811 Sequence
C 44	14.6	10.5	25	6	AX534168	AX534168 Sequence
C 45	14.6	10.5	25	6	AX534169	AX534169 Sequence
C 46	14.6	10.5	29	6	AR019082	AR019082 Sequence
C 47	14.6	10.5	30	6	AR135100	AR135100 Sequence
C 48	14.6	10.5	30	6	AX015112	AX015112 Sequence
C 49	14.6	10.5	30	6	AX611235	AX611235 Sequence
C 50	14.6	10.5	30	6	AX611566	AX611566 Sequence
C 51	14.4	10.4	20	6	AX293741	AX293741 Sequence
C 52	14.4	10.4	20	6	AX488425	AX488425 Sequence
C 53	14.4	10.4	20	6	BD171443	BD171443 Nucleic a
C 54	14.4	10.4	24	6	AX112094	AX112094 Sequence
C 55	14.4	10.4	24	6	AX289108	AX289108 Sequence
C 56	14.4	10.4	24	6	AX44387	AX44387 Sequence
C 57	14.4	10.4	25	6	AX430741	AX430741 Sequence
C 58	14.4	10.4	25	6	AX697107	AX697107 Sequence
C 59	14.4	10.4	26	6	AR061819	AR061819 Sequence
C 60	14.4	10.4	26	6	AR090522	AR090522 Sequence
C 61	14.4	10.4	26	6	AR090530	AR090530 Sequence
C 62	14.4	10.4	26	6	AR197557	AR197557 Sequence
C 63	14.4	10.4	26	6	AR197565	AR197565 Sequence
C 64	14.4	10.4	26	6	AR252810	AR252810 Sequence
C 65	14.4	10.4	26	6	AR259711	AR259711 Sequence

66	14.4	10.4	10.4	26	6	AR259719 Sequence	AR259719 Sequence	139	14	10.1	24	6	AX290661 Sequence
67	14.4	10.4	10.4	26	6	BD014707 Cyclic nu	BD014707 Cyclic nu	140	14	10.1	24	6	AX488607 Sequence
C 68	14.4	10.4	10.4	27	6	A32001 primer (S22	A32001 primer (S22	141	14	10.1	24	6	I34244 Sequence 21
C 69	14.4	10.4	10.4	27	6	AR109658 Sequence	AR109658 Sequence	C 142	14	10.1	24	6	I34245 Sequence 22
C 70	14.4	10.4	10.4	27	6	AR109660 Sequence	AR109660 Sequence	C 143	14	10.1	25	6	A84028 Sequence 15
C 71	14.4	10.4	10.4	27	6	AX175481 Sequence	AX175481 Sequence	C 144	14	10.1	25	6	AR242538 Sequence
C 72	14.4	10.4	10.4	27	6	AX537208 Sequence	AX537208 Sequence	C 145	14	10.1	25	6	AX259784 Sequence
73	14.4	10.4	10.4	28	6	AX105646 Sequence	AX105646 Sequence	C 146	14	10.1	25	6	AX534164 Sequence
74	14.4	10.4	10.4	28	6	AX108637 Sequence	AX108637 Sequence	C 147	14	10.1	25	6	BD072705 Gene conv
75	14.4	10.4	10.4	28	6	AX268878 Sequence	AX268878 Sequence	C 148	14	10.1	28	6	AX054719 Sequence
76	14.4	10.4	10.4	28	6	BD102107 A novel a	BD102107 A novel a	C 149	14	10.1	28	9	S72525 TCR V gamma
77	14.4	10.4	10.4	28	6	E48769 Novel poly	E48769 Novel poly	C 150	14	10.1	30	6	A21836 Polynucleot
78	14.4	10.4	10.4	29	6	AX588102 Sequence	AX588102 Sequence	C 151	14	10.1	30	6	AX282986 Sequence
79	14.4	10.4	10.4	29	6	AX642889 Sequence	AX642889 Sequence	C 152	14	10.1	30	6	AX703532 Sequence
C 80	14.4	10.4	10.4	30	6	A39952 Sequence 9	A39952 Sequence 9	C 153	14	10.1	30	6	BD134517 Method fo
C 81	14.4	10.4	10.4	30	6	AR000087 Sequence	AR000087 Sequence	C 154	13.8	9.9	18	6	BD074024 Human gli
C 82	14.4	10.4	10.4	30	6	AR016710 Sequence	AR016710 Sequence	C 155	13.8	9.9	20	6	AR241103 Sequence
C 83	14.4	10.4	10.4	30	6	AR016711 Sequence	AR016711 Sequence	C 156	13.8	9.9	20	6	AR281777 Sequence
C 84	14.4	10.4	10.4	30	6	AR054423 Sequence	AR054423 Sequence	C 157	13.8	9.9	20	6	AX250715 Sequence
C 85	14.4	10.4	10.4	30	6	AR064910 Sequence	AR064910 Sequence	C 158	13.8	9.9	20	6	AX253315 Sequence
C 86	14.4	10.4	10.4	30	6	AR109710 Sequence	AR109710 Sequence	C 159	13.8	9.9	20	6	AX283518 Sequence
C 87	14.4	10.4	10.4	30	6	AR243697 Sequence	AR243697 Sequence	C 160	13.8	9.9	20	6	BD006136 Methods a
C 88	14.4	10.4	10.4	30	6	I50069 Sequence 2	I50069 Sequence 2	C 161	13.8	9.9	20	6	BD179019 A method
C 89	14.4	10.4	10.4	30	6	I50070 Sequence 3	I50070 Sequence 3	C 162	13.8	9.9	22	6	AX539255 Sequence
C 90	14.4	10.4	10.4	30	6	I50106 Sequence 2	I50106 Sequence 2	C 163	13.8	9.9	22	6	AX598275 Sequence
C 91	14.4	10.4	10.4	30	6	I50107 Sequence 3	I50107 Sequence 3	C 164	13.8	9.9	25	6	A31518 Synthetic H
C 92	14.2	10.2	10.2	20	6	AR011791 Sequence	AR011791 Sequence	C 165	13.8	9.9	25	6	AX207057 Sequence
C 93	14.2	10.2	10.2	20	6	AR025499 Sequence	AR025499 Sequence	C 166	13.8	9.9	25	6	AX534163 Sequence
C 94	14.2	10.2	10.2	20	6	AR211960 Sequence	AR211960 Sequence	C 167	13.8	9.9	26	6	AR008886 Sequence
C 95	14.2	10.2	10.2	20	6	AR281496 Sequence	AR281496 Sequence	C 168	13.8	9.9	26	6	AR087581 Sequence
C 96	14.2	10.2	10.2	20	6	E08471 Primer. 9/1	E08471 Primer. 9/1	C 169	13.8	9.9	26	6	BD012117 Vitamin D
C 97	14.2	10.2	10.2	20	6	I26707 Sequence 2	I26707 Sequence 2	C 170	13.8	9.9	26	6	BD080566 MFL ligan
C 98	14.2	10.2	10.2	25	6	AR028129 Sequence	AR028129 Sequence	C 171	13.8	9.9	26	6	I85137 Sequence 11
C 99	14.2	10.2	10.2	25	6	AR030305 Sequence	AR030305 Sequence	C 172	13.8	9.9	27	6	A75720 Sequence 10
100	14.2	10.2	10.2	25	6	I42124 Sequence 19	I42124 Sequence 19	C 173	13.8	9.9	27	6	BD133033 HM74 rece
101	14.2	10.2	10.2	27	6	AR116914 Sequence	AR116914 Sequence	C 174	13.8	9.9	27	6	E06840 Oligonucleo
102	14.2	10.2	10.2	27	6	AR152252 Sequence	AR152252 Sequence	C 175	13.8	9.9	27	6	I27338 Sequence 13
103	14.2	10.2	10.2	27	6	AR154789 Sequence	AR154789 Sequence	C 176	13.8	9.9	28	6	A84070 Sequence 5
C 104	14.2	10.2	10.2	27	6	AR182531 Sequence	AR182531 Sequence	C 177	13.8	9.9	28	6	AX107824 Sequence
C 105	14.2	10.2	10.2	27	6	AX113849 Sequence	AX113849 Sequence	C 178	13.8	9.9	28	6	E41514 Reporter ge
C 106	14.2	10.2	10.2	27	6	AX116588 Sequence	AX116588 Sequence	C 179	13.8	9.9	29	6	A68741 Sequence 3
C 107	14.2	10.2	10.2	27	6	AX117036 Sequence	AX117036 Sequence	C 180	13.8	9.9	29	6	AR016276 Sequence
C 108	14.2	10.2	10.2	27	6	AX304425 Sequence	AX304425 Sequence	C 181	13.8	9.9	29	6	AX003396 Sequence
C 109	14.2	10.2	10.2	27	6	AX451838 Sequence	AX451838 Sequence	C 182	13.8	9.9	29	6	AX118458 Sequence
C 110	14.2	10.2	10.2	27	6	BD074012 Method fo	BD074012 Method fo	C 183	13.8	9.9	29	6	AX328910 Sequence
C 111	14.2	10.2	10.2	28	6	AR265212 Sequence	AR265212 Sequence	C 184	13.8	9.9	29	6	AX339538 Sequence
C 112	14.2	10.2	10.2	28	6	AX339688 Sequence	AX339688 Sequence	C 185	13.8	9.9	29	6	AX503502 Sequence
C 113	14.2	10.2	10.2	28	6	AX351768 Sequence	AX351768 Sequence	C 186	13.8	9.9	29	6	BD086260 Vector. 8
C 114	14.2	10.2	10.2	28	6	AX458824 Sequence	AX458824 Sequence	C 187	13.8	9.9	29	6	BD177691 Process f
C 115	14.2	10.2	10.2	29	6	AR012146 Sequence	AR012146 Sequence	C 188	13.8	9.9	29	6	E12841 PCR primer
C 116	14.2	10.2	10.2	29	6	AR091248 Sequence	AR091248 Sequence	C 189	13.8	9.9	30	6	AR011576 Sequence
C 117	14.2	10.2	10.2	29	6	AR198283 Sequence	AR198283 Sequence	C 190	13.8	9.9	30	6	AR080447 Sequence
C 118	14.2	10.2	10.2	29	6	AR260437 Sequence	AR260437 Sequence	C 191	13.8	9.9	30	6	AR111511 Sequence
C 119	14.2	10.2	10.2	30	6	AR024460 Sequence	AR024460 Sequence	C 192	13.8	9.9	30	6	AR181111 Sequence
C 120	14.2	10.2	10.2	30	6	AR176004 Sequence	AR176004 Sequence	C 193	13.8	9.9	30	6	AX310734 Sequence
C 121	14.2	10.2	10.2	30	6	AR308620 Sequence	AR308620 Sequence	C 194	13.8	9.9	30	6	AX148786 Sequence
C 122	14.2	10.2	10.2	30	6	AR308639 Sequence	AR308639 Sequence	C 195	13.8	9.9	30	6	BD022388 Sequence
C 123	14.2	10.2	10.2	30	6	AX006692 Sequence	AX006692 Sequence	C 196	13.8	9.9	30	6	BD069819 Dendritic
C 124	14.2	10.2	10.2	30	6	AX009400 Sequence	AX009400 Sequence	C 197	13.8	9.9	30	6	I18214 Sequence 45
C 125	14.2	10.2	10.2	30	6	AX155549 Sequence	AX155549 Sequence	C 198	13.8	9.9	30	7	PFDFRGMTZ
C 126	14.2	10.2	10.2	30	6	AX472252 Sequence	AX472252 Sequence	C 199	13.6	9.8	20	6	A98445 Sequence 29
C 127	14.2	10.2	10.2	30	6	AX611465 Sequence	AX611465 Sequence	C 200	13.6	9.8	20	6	AR050289 Sequence
C 128	14.2	10.2	10.2	30	6	AX611467 Sequence	AX611467 Sequence	C 201	13.6	9.8	20	6	AR100579 Sequence
C 129	14.2	10.2	10.2	30	6	AX611469 Sequence	AX611469 Sequence	C 202	13.6	9.8	20	6	AR100585 Sequence
C 130	14.2	10.2	10.2	30	6	AX611470 Sequence	AX611470 Sequence	C 203	13.6	9.8	20	6	AR158965 Sequence
C 131	14.2	10.2	10.2	30	6	AX694371 Sequence	AX694371 Sequence	C 204	13.6	9.8	20	6	AR298667 Sequence
C 132	14.2	10.2	10.2	30	6	I63333 Sequence 14	I63333 Sequence 14	C 205	13.6	9.8	20	6	AR316120 Sequence
C 133	14	10.1	10.1	20	6	A63347 oligonucleo	A63347 oligonucleo	C 206	13.6	9.8	20	6	AR316177 Sequence
C 134	14	10.1	10.1	22	6	A94117 Sequence 98	A94117 Sequence 98	C 207	13.6	9.8	20	6	AX115823 Sequence
C 135	14	10.1	10.1	22	6	AR232639 Sequence	AR232639 Sequence	C 208	13.6	9.8	20	6	BD144090 Method fo
C 136	14	10.1	10.1	22	6	AX011202 Sequence	AX011202 Sequence	C 209	13.6	9.8	20	6	E26692 Improved me
C 137	14	10.1	10.1	23	6	AX327669 Sequence	AX327669 Sequence	C 210	13.6	9.8	20	6	I31522 Sequence 43
C 138	14	10.1	10.1	23	6	AX452265 Sequence	AX452265 Sequence	C 211	13.6	9.8	21	6	AR278808 Sequence

C 212	13.6	9.8	21	6	AX589272	AX589272 Sequence
C 213	13.6	9.8	22	6	AX033204	AX033204 Sequence
C 214	13.6	9.8	23	6	A61986	A61986 Sequence 16
C 215	13.6	9.8	23	6	AX487068	AX487068 Sequence
C 216	13.6	9.8	23	6	BD061613	BD061613 Human Laf
C 217	13.6	9.8	24	6	AR095625	AR095625 Sequence
C 218	13.6	9.8	24	6	AX106733	AX106733 Sequence
C 219	13.6	9.8	24	6	AX446180	AX446180 Sequence
C 220	13.6	9.8	24	6	AX446782	AX446782 Sequence
C 221	13.6	9.8	24	6	AX683626	AX683626 Sequence
C 222	13.6	9.8	24	6	E49254	E49254 Omega 3 fat
C 223	13.6	9.8	25	6	A37998	A37998 Sequence 5
C 224	13.6	9.8	25	6	AR059422	AR059422 Sequence
C 225	13.6	9.8	25	6	AR285452	AR285452 Sequence
C 226	13.6	9.8	25	6	AR287486	AR287486 Sequence
C 227	13.6	9.8	25	6	AR307720	AR307720 Sequence
C 228	13.6	9.8	25	6	AX001355	AX001355 Sequence
C 229	13.6	9.8	25	6	AX534170	AX534170 Sequence
C 230	13.6	9.8	25	6	AX590588	AX590588 Sequence
C 231	13.6	9.8	25	6	BD000284	BD000284 cdna comp
C 232	13.6	9.8	25	6	I22220	I22220 Sequence 1
C 233	13.6	9.8	26	6	BD000254	BD000254 Oligonucl
C 234	13.6	9.8	26	6	BD000351	BD000351 Method fo
C 235	13.6	9.8	27	6	AR071913	AR071913 Sequence
C 236	13.6	9.8	27	6	AR279431	AR279431 Sequence
C 237	13.6	9.8	27	6	BD097281	BD097281 Novel col
C 238	13.6	9.8	27	6	BD097291	BD097291 Novel col
C 239	13.6	9.8	28	6	AR198664	AR198664 Sequence
C 240	13.6	9.8	28	6	AX350231	AX350231 Sequence
C 241	13.6	9.8	28	6	I62302	I62302 Sequence 13
C 242	13.6	9.8	29	6	AR221982	AR221982 Sequence
C 243	13.6	9.8	29	6	AX000864	AX000864 Sequence
C 244	13.6	9.8	29	6	AX000864	AX000864 Sequence
C 245	13.6	9.8	29	6	AX304421	AX304421 Sequence
C 246	13.6	9.8	30	6	A51853	A51853 Sequence 17
C 247	13.6	9.8	30	6	A51857	A51857 Sequence 21
C 248	13.6	9.8	30	6	AR058826	AR058826 Sequence
C 249	13.6	9.8	30	6	AR125828	AR125828 Sequence
C 250	13.6	9.8	30	6	AR262364	AR262364 Sequence
C 251	13.6	9.8	30	6	AX028493	AX028493 Sequence
C 252	13.6	9.8	30	6	AX431446	AX431446 Sequence
C 253	13.6	9.8	30	6	E07788	E07788 PCR primer
C 254	13.6	9.8	30	6	I47240	I47240 Sequence 17
C 255	13.4	9.6	17	6	AX723714	AX723714 Sequence
C 256	13.4	9.6	18	6	AX352825	AX352825 Sequence
C 257	13.4	9.6	18	6	AX362670	AX362670 Sequence
C 258	13.4	9.6	18	12	AB069639	AB069639 Synthetic
C 259	13.4	9.6	19	6	AX129291	AX129291 Sequence
C 260	13.4	9.6	19	6	BD088226	BD088226 A method
C 261	13.4	9.6	19	6	BD088234	BD088234 A method
C 262	13.4	9.6	19	12	AB069135	AB069135 Synthetic
C 263	13.4	9.6	19	12	AB069137	AB069137 Synthetic
C 264	13.4	9.6	20	6	AR163797	AR163797 Sequence
C 265	13.4	9.6	21	6	E08711	E08711 Probe for d
C 266	13.4	9.6	22	6	AX742721	AX742721 Sequence
C 267	13.4	9.6	22	6	AX742722	AX742722 Sequence
C 268	13.4	9.6	23	6	AR037776	AR037776 Sequence
C 269	13.4	9.6	23	6	AR037853	AR037853 Sequence
C 270	13.4	9.6	23	6	AR069386	AR069386 Sequence
C 271	13.4	9.6	23	6	AR081603	AR081603 Sequence
C 272	13.4	9.6	23	6	BD133242	BD133242 Polymeras
C 273	13.4	9.6	23	6	BD176902	BD176902 Gene enco
C 274	13.4	9.6	24	6	AX072270	AX072270 Sequence
C 275	13.4	9.6	24	6	AX089577	AX089577 Sequence
C 276	13.4	9.6	24	6	AX117886	AX117886 Sequence
C 277	13.4	9.6	24	6	AX327692	AX327692 Sequence
C 278	13.4	9.6	24	6	AX528500	AX528500 Sequence
C 279	13.4	9.6	24	6	E31858	E31858 Novel cance
C 280	13.4	9.6	24	6	I26381	I26381 Sequence 73
C 281	13.4	9.6	25	6	A27612	A27612 p150 Gene
C 282	13.4	9.6	25	6	AR026123	AR026123 Sequence
C 283	13.4	9.6	25	6	AX166665	AX166665 Sequence
C 284	13.4	9.6	25	6	AX196787	AX196787 Sequence
C 285	13.4	9.6	25	6	AX501645	AX501645 Sequence
C 286	13.4	9.6	25	6	AX501646	AX501646 Sequence
C 287	13.4	9.6	25	6	AX501647	AX501647 Sequence
C 288	13.4	9.6	25	6	AX534161	AX534161 Sequence
C 289	13.4	9.6	25	6	AX534162	AX534162 Sequence
C 290	13.4	9.6	25	6	AX534516	AX534516 Sequence
C 291	13.4	9.6	25	6	AX534517	AX534517 Sequence
C 292	13.4	9.6	25	6	AX534518	AX534518 Sequence
C 293	13.4	9.6	25	6	AX610814	AX610814 Sequence
C 294	13.4	9.6	25	6	AX650380	AX650380 Sequence
C 295	13.4	9.6	25	6	AX650381	AX650381 Sequence
C 296	13.4	9.6	25	6	AX650382	AX650382 Sequence
C 297	13.4	9.6	25	6	AX675457	AX675457 Sequence
C 298	13.4	9.6	25	6	AX689063	AX689063 Sequence
C 299	13.4	9.6	25	6	AX689064	AX689064 Sequence
C 300	13.4	9.6	25	6	AX689065	AX689065 Sequence
C 301	13.4	9.6	25	6	BD015394	BD015394 Method fo
C 302	13.4	9.6	25	6	BD095604	BD095604 Method fo
C 303	13.4	9.6	25	6	BD1411307	BD1411307 Method of
C 304	13.4	9.6	25	6	E10529	E10529 N-terminal
C 305	13.4	9.6	25	6	E26156	E26156 Novel brain
C 306	13.4	9.6	25	11	C75924	C75924 Homo sapien
C 307	13.4	9.6	26	6	AX037903	AX037903 Sequence
C 308	13.4	9.6	26	6	AX060334	AX060334 Sequence
C 309	13.4	9.6	27	6	AR090434	AR090434 Sequence
C 310	13.4	9.6	27	6	AR109595	AR109595 Sequence
C 311	13.4	9.6	27	6	AR109652	AR109652 Sequence
C 312	13.4	9.6	27	6	AR150643	AR150643 Sequence
C 313	13.4	9.6	27	6	AR197469	AR197469 Sequence
C 314	13.4	9.6	27	6	AR211515	AR211515 Sequence
C 315	13.4	9.6	27	6	AR254612	AR254612 Sequence
C 316	13.4	9.6	27	6	AR259623	AR259623 Sequence
C 317	13.4	9.6	27	6	AR266284	AR266284 Sequence
C 318	13.4	9.6	27	6	AR300905	AR300905 Sequence
C 319	13.4	9.6	27	6	AX107993	AX107993 Sequence
C 320	13.4	9.6	27	6	AX343819	AX343819 Sequence
C 321	13.4	9.6	27	6	AX343820	AX343820 Sequence
C 322	13.4	9.6	27	6	E11748	E11748 Primer for
C 323	13.4	9.6	27	6	E12466	E12466 PCR primer
C 324	13.4	9.6	27	6	E12660	E12660 Primer. 4/1
C 325	13.4	9.6	27	6	E14221	E14221 Primer. 7/1
C 326	13.4	9.6	27	6	E16192	E16192 Primer. 7/1
C 327	13.4	9.6	27	6	E27218	E27218 Novel physi
C 328	13.4	9.6	27	6	E28276	E28276 Utilization
C 329	13.4	9.6	27	6	E37242	E37242 Novel physi
C 330	13.4	9.6	28	6	BD173733	BD173733 Use of ga
C 331	13.4	9.6	28	6	E39416	E39416 Novel physi
C 332	13.4	9.6	28	6	AX023345	AX023345 Sequence
C 333	13.4	9.6	29	6	AR028303	AR028303 Sequence
C 334	13.4	9.6	30	6	AR308640	AR308640 Sequence
C 335	13.4	9.6	30	6	AX174690	AX174690 Sequence
C 336	13.4	9.6	29	6	AX161337	AX161337 Sequence
C 337	13.4	9.6	29	6	BD063660	BD063660 Nucleotid
C 338	13.4	9.6	29	6	BD063661	BD063661 Nucleotid
C 339	13.4	9.6	30	6	A43131	A43131 Sequence 17
C 340	13.4	9.6	30	6	AR028303	AR028303 Sequence
C 341	13.4	9.6	30	6	AX063377	AX063377 Sequence
C 342	13.4	9.6	30	6	AX590524	AX590524 Sequence
C 343	13.4	9.6	30	6	BD004770	BD004770 Novel VEG
C 344	13.4	9.6	30	6	BD141184	BD141184 Novel G p
C 345	13.4	9.6	30	6	BD168845	BD168845 Antibody
C 346	13.4	9.6	30	6	E31709	E31709 Method for
C 347	13.4	9.6	30	9	HUMPLTP06	U37813 Human phosph
C 348	13.2	9.5	18	6	A63088	A63088 Sequence 15
C 349	13.2	9.5	18	6	AR018185	AR018185 Sequence
C 350	13.2	9.5	18	6	AR106914	AR106914 Sequence
C 351	13.2	9.5	18	6	AR173918	AR173918 Sequence
C 352	13.2	9.5	18	6	AR268665	AR268665 Sequence
C 353	13.2	9.5	18	6	BD089837	BD089837 A method
C 354	13.2	9.5	18	12	AB068204	AB068204 Synthetic
C 355	13.2	9.5	19	6	AR011803	AR011803 Sequence
C 356	13.2	9.5	20	6	A70767	A70767 Sequence 88
C 357	13.2	9.5	20	6	A79251	A79251 Sequence 88
C 358	13.2	9.5	20	6	AR163916	AR163916 Sequence

C 358	13.2	9.5	20	6	AR220154 Sequence	C 431	13.2	9.5	28	6	AR120088 Sequence
C 359	13.2	9.5	20	6	AR315612 Sequence	432	13.2	9.5	28	6	AR120089 Sequence
C 360	13.2	9.5	20	6	AX180379 Sequence	C 433	13.2	9.5	28	6	AR258737 Sequence
C 361	13.2	9.5	20	6	AX268920 Sequence	434	13.2	9.5	28	6	AX001136 Sequence
C 362	13.2	9.5	20	6	AX287952 Sequence	C 435	13.2	9.5	28	6	AX092072 Sequence
C 363	13.2	9.5	20	6	BD003481 Sequence	C 436	13.2	9.5	28	6	AX092090 Sequence
C 364	13.2	9.5	20	6	BD011678 Sequence	C 437	13.2	9.5	28	6	AX092173 Sequence
C 365	13.2	9.5	20	6	BD011679 Method fo	C 438	13.2	9.5	28	6	AX092896 Sequence
C 366	13.2	9.5	20	6	BD011680 Method fo	C 439	13.2	9.5	28	6	BD085055 Laundry a
C 367	13.2	9.5	20	6	E08376 Primer for	C 440	13.2	9.5	28	6	189994 Sequence 7
C 368	13.2	9.5	20	6	AR084364 Sequence	441	13.2	9.5	29	6	AI17044 oligonucleo
C 369	13.2	9.5	21	6	AR265767 Sequence	442	13.2	9.5	29	6	AI17444 oligonucleo
C 370	13.2	9.5	21	6	AR295668 Sequence	443	13.2	9.5	29	6	A23876 mutagenic o
C 371	13.2	9.5	21	6	AR096170 Sequence	444	13.2	9.5	29	6	AR014419 Sequence
C 372	13.2	9.5	21	6	AX546835 Sequence	445	13.2	9.5	29	6	AR059821 Sequence
C 373	13.2	9.5	21	6	AX555005 Sequence	446	13.2	9.5	29	6	AR061350 Sequence
C 374	13.2	9.5	21	6	AX662973 Sequence	447	13.2	9.5	29	6	AR108249 Sequence
C 375	13.2	9.5	21	6	AX696117 Sequence	448	13.2	9.5	29	6	AR176253 Sequence
C 376	13.2	9.5	21	6	I26653 Sequence 20	449	13.2	9.5	29	6	AR263210 Sequence
C 377	13.2	9.5	22	6	AX059300 Sequence	C 450	13.2	9.5	29	6	AR265213 Sequence
C 378	13.2	9.5	22	6	AX211674 Sequence	C 451	13.2	9.5	29	6	AR265222 Sequence
C 379	13.2	9.5	23	6	AR210375 Sequence	452	13.2	9.5	29	6	AX003166 Sequence
C 380	13.2	9.5	24	6	AR072270 Sequence	453	13.2	9.5	29	6	AX023711 Sequence
C 381	13.2	9.5	24	6	AR096578 Sequence	C 454	13.2	9.5	29	6	AX203048 Sequence
C 382	13.2	9.5	24	6	AR105954 Sequence	455	13.2	9.5	29	6	AX326794 Sequence
C 383	13.2	9.5	24	6	AR216925 Sequence	456	13.2	9.5	29	6	AX429101 Sequence
C 384	13.2	9.5	24	6	AX444219 Sequence	457	13.2	9.5	29	6	AX452346 Sequence
C 385	13.2	9.5	24	6	AX446815 Sequence	458	13.2	9.5	29	6	AX658977 Sequence
C 386	13.2	9.5	24	6	AX446869 Sequence	459	13.2	9.5	29	6	AX658977 Sequence
C 387	13.2	9.5	24	6	AX574695 Sequence	460	13.2	9.5	29	6	BD105436 Method fo
C 388	13.2	9.5	24	6	BD086394 KCNQ2 and	461	13.2	9.5	29	6	I11862 Sequence 28
C 389	13.2	9.5	24	6	I26381 Sequence 73	462	13.2	9.5	29	6	I16206 Sequence 32
C 390	13.2	9.5	25	6	A25985 Artificial	463	13.2	9.5	29	6	I66692 Sequence 32
C 391	13.2	9.5	25	6	AR243397 Sequence	464	13.2	9.5	29	6	I84786 Sequence 32
C 392	13.2	9.5	25	6	AX115344 Sequence	465	13.2	9.5	30	6	AR099298 Sequence
C 393	13.2	9.5	25	6	AX116752 Sequence	466	13.2	9.5	30	6	AR172505 Sequence
C 394	13.2	9.5	25	6	AX448185 Sequence	C 467	13.2	9.5	30	6	AR204083 Sequence
C 395	13.2	9.5	25	6	AX534316 Sequence	C 468	13.2	9.5	30	6	AX039277 Sequence
C 396	13.2	9.5	25	6	AX534317 Sequence	469	13.2	9.5	30	6	AX451790 Sequence
C 397	13.2	9.5	25	6	AX534318 Sequence	C 470	13.2	9.5	30	6	BD077089 Sequence
C 398	13.2	9.5	25	6	AX534319 Sequence	C 471	13.2	9.5	30	9	HSTCRGV22
C 399	13.2	9.5	25	6	AX534320 Sequence	C 472	13.2	9.5	21	6	AR8019 Sequence 49
C 400	13.2	9.5	25	6	AX534321 Sequence	473	13.2	9.5	21	6	AR178428 Sequence
C 401	13.2	9.5	25	6	AX534322 Sequence	474	13.2	9.5	21	6	AR209729 Sequence
C 402	13.2	9.5	25	6	AX534323 Sequence	475	13.2	9.5	21	6	AR217679 Sequence
C 403	13.2	9.5	25	6	AX548324 Sequence	C 476	13.2	9.5	21	6	AR255703 Sequence
C 404	13.2	9.5	25	6	BD011127 Human tel	477	13.2	9.5	21	6	AX059305 Sequence
C 405	13.2	9.5	25	6	E33489 Apoptosis-r	C 478	13.2	9.5	21	6	AX118828 Sequence
C 406	13.2	9.5	25	6	E36876 Human telom	C 479	13.2	9.5	21	6	AX391237 Sequence
C 407	13.2	9.5	26	6	A42206 Sequence 96	480	13.2	9.5	21	6	AX399562 Sequence
C 408	13.2	9.5	26	6	AR004850 Sequence	481	13.2	9.5	21	6	BD089458 A method
C 409	13.2	9.5	26	6	AR090229 Sequence	482	13.2	9.5	21	6	BD181112 Human DNA
C 410	13.2	9.5	26	6	AR197264 Sequence	C 483	13.2	9.5	21	12	AB068283 Synthetic
C 411	13.2	9.5	26	6	AR252542 Sequence	C 484	13.2	9.5	22	6	AR169915 Sequence
C 412	13.2	9.5	26	6	AR259418 Sequence	C 485	13.2	9.5	22	6	AR172619 Sequence
C 413	13.2	9.5	26	6	AR271499 Sequence	C 486	13.2	9.5	22	6	AX111355 Sequence
C 414	13.2	9.5	26	6	AX067207 Sequence	C 487	13.2	9.5	22	6	AX298056 Sequence
C 415	13.2	9.5	26	6	AX286045 Sequence	C 488	13.2	9.5	22	6	AX577803 Sequence
C 416	13.2	9.5	26	6	AX403355 Sequence	C 489	13.2	9.5	22	6	AX717035 Sequence
C 417	13.2	9.5	26	6	BD135973 Methods f	490	13.2	9.5	23	6	AX2413 Sequence 38
C 418	13.2	9.5	26	6	I71256 Sequence 53	C 491	13.2	9.5	23	6	AR109812 Sequence
C 419	13.2	9.5	27	6	AR005179 Sequence	492	13.2	9.5	23	6	AR268414 Sequence
C 420	13.2	9.5	27	6	AR038389 Sequence	C 493	13.2	9.5	23	6	AR306337 Sequence
C 421	13.2	9.5	27	6	AR178125 Sequence	494	13.2	9.5	23	6	AX600955 Sequence
C 422	13.2	9.5	27	6	AX278644 Sequence	C 495	13.2	9.5	24	6	AX015893 Sequence
C 423	13.2	9.5	27	6	AX614426 Sequence	496	13.2	9.5	24	6	AX028889 Sequence
C 424	13.2	9.5	27	6	BD004780 Novel VEG	497	13.2	9.5	24	6	AX173358 Sequence
C 425	13.2	9.5	27	6	BD068730 Enzymatic	C 498	13.2	9.5	24	6	AX450599 Sequence
C 426	13.2	9.5	27	6	BD091903 Recombina	499	13.2	9.5	24	6	AX445340 Sequence
C 427	13.2	9.5	27	6	BD168855 Antibody	500	13.2	9.5	24	6	AX445918 Sequence
C 428	13.2	9.5	27	6	I58465 Sequence 36	501	13.2	9.5	24	6	AX446896 Sequence
C 429	13.2	9.5	27	6	I66583 Sequence 36	502	13.2	9.5	24	6	BD090070 A method
C 430	13.2	9.5	27	6	I68230 Sequence 36	503	13.2	9.5	24	12	AB068633 Synthetic

504	13	9.4	25	6	AR026123	Sequence	AR026123	Sequence	577	13	9.4	30	6	AX611567	Sequence
505	13	9.4	25	6	AR184037	Sequence	AR184037	Sequence	c 578	13	9.4	30	6	BD057904	Death dom
506	13	9.4	25	6	AX115096	Sequence	AX115096	Sequence	579	13	9.4	30	6	BD140224	Cultivar-
507	13	9.4	25	6	AX511780	Sequence	AX511780	Sequence	c 580	13	9.4	30	6	BD173888	BD173888 Receptor
508	13	9.4	25	6	AX534159	Sequence	AX534159	Sequence	581	13	9.4	30	6	BD173888	BD173888 Receptor
509	13	9.4	25	6	AX534160	Sequence	AX534160	Sequence	c 582	13	9.4	30	6	AX611567	Sequence
510	13	9.4	25	6	AX534514	Sequence	AX534514	Sequence	583	12.8	9.2	16	6	AX710950	Sequence
511	13	9.4	25	6	AX534515	Sequence	AX534515	Sequence	584	12.8	9.2	16	6	BD001091	Method an
512	13	9.4	25	6	AX689061	Sequence	AX689061	Sequence	585	12.8	9.2	16	6	BD001520	Method an
513	13	9.4	25	6	AX689062	Sequence	AX689062	Sequence	c 586	12.8	9.2	17	6	AR011799	Sequence
514	13	9.4	25	6	AX689465	Sequence	AX689465	Sequence	587	12.8	9.2	17	6	AR192421	Sequence
515	13	9.4	25	6	AX689466	Sequence	AX689466	Sequence	c 588	12.8	9.2	17	6	AX421994	Sequence
516	13	9.4	25	6	AX689467	Sequence	AX689467	Sequence	c 589	12.8	9.2	17	6	AX422971	Sequence
517	13	9.4	25	6	AX689468	Sequence	AX689468	Sequence	c 590	12.8	9.2	17	6	AX673768	Sequence
518	13	9.4	25	6	AX689469	Sequence	AX689469	Sequence	c 591	12.8	9.2	17	6	AX724290	Sequence
519	13	9.4	25	6	BD014482	Transgeni	BD014482	Transgeni	c 592	12.8	9.2	18	6	BD104946	Kit and m
520	13	9.4	25	6	BD103612	Peptide a	BD103612	Peptide a	c 593	12.8	9.2	18	6	AR011802	Sequence
521	13	9.4	25	6	BD103621	Peptide a	BD103621	Peptide a	c 594	12.8	9.2	18	6	AR051200	Sequence
522	13	9.4	25	6	BD161876	KI gene.	BD161876	KI gene.	595	12.8	9.2	18	6	AR106948	Sequence
523	13	9.4	25	6	E31296	Monoclonal	E31296	Monoclonal	596	12.8	9.2	18	6	AR106981	Sequence
524	13	9.4	25	6	I09525	Sequence 9	I09525	Sequence 9	597	12.8	9.2	19	6	AX129110	Sequence
525	13	9.4	25	6	I21606	Sequence 17	I21606	Sequence 17	c 598	12.8	9.2	19	11	DOGCTRB	Sequence
526	13	9.4	25	6	I68675	Sequence 40	I68675	Sequence 40	c 599	12.8	9.2	20	6	AR011789	Sequence
527	13	9.4	25	6	E17354	PCR primer	E17354	PCR primer	600	12.8	9.2	20	6	AR158819	Sequence
528	13	9.4	25	6	AR109655	Sequence	AR109655	Sequence	601	12.8	9.2	20	6	AR158820	Sequence
529	13	9.4	25	6	AR143767	Sequence	AR143767	Sequence	602	12.8	9.2	20	6	AR158821	Sequence
530	13	9.4	25	6	AR144854	Sequence	AR144854	Sequence	603	12.8	9.2	20	6	AR158822	Sequence
531	13	9.4	25	6	AR144855	Sequence	AR144855	Sequence	604	12.8	9.2	20	6	AR158823	Sequence
532	13	9.4	25	6	AR196640	Sequence	AR196640	Sequence	605	12.8	9.2	20	6	AR295189	Sequence
533	13	9.4	25	6	AX148320	Sequence	AX148320	Sequence	606	12.8	9.2	20	6	AR313974	Sequence
534	13	9.4	25	6	AX191943	Sequence	AX191943	Sequence	607	12.8	9.2	20	6	AX298771	Sequence
535	13	9.4	25	6	BD017438	Transgeni	BD017438	Transgeni	c 608	12.8	9.2	20	6	AX326898	Sequence
536	13	9.4	25	6	BD131675	Carcinoem	BD131675	Carcinoem	609	12.8	9.2	20	6	AX326958	Sequence
537	13	9.4	25	6	BD145135	Method fo	BD145135	Method fo	610	12.8	9.2	20	6	AX326958	Sequence
538	13	9.4	25	6	I91810	Sequence 12	I91810	Sequence 12	611	12.8	9.2	20	6	AX326958	Sequence
539	13	9.4	25	6	I91991	Sequence 12	I91991	Sequence 12	612	12.8	9.2	20	6	AX326958	Sequence
540	13	9.4	25	6	AR106112	Sequence	AR106112	Sequence	c 613	12.8	9.2	20	6	AX326958	Sequence
541	13	9.4	25	6	AX461497	Sequence	AX461497	Sequence	614	12.8	9.2	20	6	AX326958	Sequence
542	13	9.4	25	6	AX575781	Sequence	AX575781	Sequence	615	12.8	9.2	20	6	AX326958	Sequence
543	13	9.4	25	6	BD102639	Compositi	BD102639	Compositi	616	12.8	9.2	20	6	AX326958	Sequence
544	13	9.4	25	6	AR303245	Sequence	AR303245	Sequence	617	12.8	9.2	20	6	AX326958	Sequence
545	13	9.4	25	6	AX166369	Sequence	AX166369	Sequence	618	12.8	9.2	20	6	AX326958	Sequence
546	13	9.4	25	6	AX252352	Sequence	AX252352	Sequence	619	12.8	9.2	20	6	AX326958	Sequence
547	13	9.4	25	6	AX375451	Sequence	AX375451	Sequence	620	12.8	9.2	20	6	AX326958	Sequence
548	13	9.4	25	6	BD106424	Secreted	BD106424	Secreted	621	12.8	9.2	20	6	AX326958	Sequence
549	13	9.4	25	6	BD136025	Secretory	BD136025	Secretory	622	12.8	9.2	20	6	AX326958	Sequence
550	13	9.4	25	6	I50760	Sequence 5	I50760	Sequence 5	623	12.8	9.2	20	6	AX326958	Sequence
551	13	9.4	25	6	AR000087	Sequence	AR000087	Sequence	624	12.8	9.2	20	6	AX326958	Sequence
552	13	9.4	25	6	AR018187	Sequence	AR018187	Sequence	625	12.8	9.2	20	6	AX326958	Sequence
553	13	9.4	25	6	AR064910	Sequence	AR064910	Sequence	626	12.8	9.2	20	6	AX326958	Sequence
554	13	9.4	25	6	AR067287	Sequence	AR067287	Sequence	627	12.8	9.2	20	6	AX326958	Sequence
555	13	9.4	25	6	AR068857	Sequence	AR068857	Sequence	628	12.8	9.2	20	6	AX326958	Sequence
556	13	9.4	25	6	AR070157	Sequence	AR070157	Sequence	629	12.8	9.2	20	6	AX326958	Sequence
557	13	9.4	25	6	AR102892	Sequence	AR102892	Sequence	630	12.8	9.2	20	6	AX326958	Sequence
558	13	9.4	25	6	AR108071	Sequence	AR108071	Sequence	631	12.8	9.2	20	6	AX326958	Sequence
559	13	9.4	25	6	AR109700	Sequence	AR109700	Sequence	632	12.8	9.2	20	6	AX326958	Sequence
560	13	9.4	25	6	AR125895	Sequence	AR125895	Sequence	633	12.8	9.2	20	6	AX326958	Sequence
561	13	9.4	25	6	AR134719	Sequence	AR134719	Sequence	634	12.8	9.2	20	6	AX326958	Sequence
562	13	9.4	25	6	AX019521	Sequence	AX019521	Sequence	635	12.8	9.2	20	6	AX326958	Sequence
563	13	9.4	25	6	AX085661	Sequence	AX085661	Sequence	636	12.8	9.2	20	6	AX326958	Sequence
564	13	9.4	25	6	AX304841	Sequence	AX304841	Sequence	637	12.8	9.2	20	6	AX326958	Sequence
565	13	9.4	25	6	AX427970	Sequence	AX427970	Sequence	638	12.8	9.2	20	6	AX326958	Sequence
566	13	9.4	25	6	AX431446	Sequence	AX431446	Sequence	639	12.8	9.2	20	6	AX326958	Sequence
567	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	640	12.8	9.2	20	6	AX326958	Sequence
568	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	641	12.8	9.2	20	6	AX326958	Sequence
569	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	642	12.8	9.2	20	6	AX326958	Sequence
570	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	643	12.8	9.2	20	6	AX326958	Sequence
571	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	644	12.8	9.2	20	6	AX326958	Sequence
572	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	645	12.8	9.2	20	6	AX326958	Sequence
573	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	646	12.8	9.2	20	6	AX326958	Sequence
574	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	647	12.8	9.2	20	6	AX326958	Sequence
575	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	648	12.8	9.2	20	6	AX326958	Sequence
576	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	649	12.8	9.2	20	6	AX326958	Sequence
577	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	650	12.8	9.2	20	6	AX326958	Sequence
578	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	651	12.8	9.2	20	6	AX326958	Sequence
579	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	652	12.8	9.2	20	6	AX326958	Sequence
580	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	653	12.8	9.2	20	6	AX326958	Sequence
581	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	654	12.8	9.2	20	6	AX326958	Sequence
582	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	655	12.8	9.2	20	6	AX326958	Sequence
583	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	656	12.8	9.2	20	6	AX326958	Sequence
584	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	657	12.8	9.2	20	6	AX326958	Sequence
585	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	658	12.8	9.2	20	6	AX326958	Sequence
586	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	659	12.8	9.2	20	6	AX326958	Sequence
587	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	660	12.8	9.2	20	6	AX326958	Sequence
588	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	661	12.8	9.2	20	6	AX326958	Sequence
589	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	662	12.8	9.2	20	6	AX326958	Sequence
590	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	663	12.8	9.2	20	6	AX326958	Sequence
591	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	664	12.8	9.2	20	6	AX326958	Sequence
592	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	665	12.8	9.2	20	6	AX326958	Sequence
593	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	666	12.8	9.2	20	6	AX326958	Sequence
594	13	9.4	25	6	AX611234	Sequence	AX611234	Sequence	667	12.8	9.2	20	6	AX326958	Sequence
595	13	9.4	25	6	AX611234										

STYON TREAT

```
source
1..21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
2 a 9 c 2 g 8 t
BASE COUNT
ORIGIN
Query Match
Best Local Similarity 12.1%; Score 16.8; DB 6; Length 21;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 102 TTGGCTCCCACTCCCTCCT 121
DB 1 TTGGCTCCCACTCCCTCCT 20
RESULT 6
AR262363
LOCUS
DEFINITION
Sequence 1 from patent US 6323179.
ACCESSION
AR262363
VERSION
AR262363.1 GI:28073792
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Siler-Khodr, T.
TITLE
Chicken GNRH analogs and uses thereof in regulation of fertility
and pregnancy
JOURNAL
Patent: US 6323179-A 1 27-NOV-2001;
FEATURES
Location/Qualifiers
1..30
source
/organism="unknown"
BASE COUNT
5 a 8 c 9 g 8 t
ORIGIN
Query Match
Best Local Similarity 12.1%; Score 16.8; DB 6; Length 30;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 25 AGCACCAGGCTCACAGCTGGAACCTGG 52
DB 2 AGCAGTGGTCTCATGGCTGGTATCTGG 29
RESULT 7
AR129513
LOCUS
DEFINITION
Sequence 102 from patent US 6187533.
ACCESSION
AR129513
VERSION
AR129513.1 GI:14117410
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 22)
AUTHORS
Bell, G. I., Yamagata, K., Oda, N., Kaisaki, P. J., Furuta, H.,
Horikawa, Y., and Menzel, S.
TITLE
Mutations in the diabetes susceptibility genes hepatocyte nuclear
factor (HNF) 1 alpha (alpha.), HNF1beta, and HNF4alpha
JOURNAL
Patent: US 6187533-A 102 13-FEB-2001;
FEATURES
Location/Qualifiers
1..22
source
/organism="unknown"
BASE COUNT
8 a 9 c 3 g 2 t
ORIGIN
Query Match
Best Local Similarity 11.7%; Score 16.2; DB 6; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 28 ACCAGGCTCACAGCTGGAACCT 48
Db
|||||
2 ACCAGGCTCACAGCTGGAACCT 22
RESULT 8
E24992
LOCUS
DEFINITION
28 bp DNA linear PAT 18-JUN-2001
Apoptosis-inhibiting protein, gene encoding the same and cDNA
thereof.
E24992
ACCESSION
E24992.1 GI:13024690
VERSION
JP 1999116599-A/4.
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 28)
AUTHORS
Shigehiro, I. and Kenji, Y.
TITLE
Apoptosis-inhibiting protein, gene encoding the same and cDNA
Patent: JP 1999116599-A 4 27-APR-1999;
JOURNAL
SCIENCE & TECH AGENCY
COMMENT
OS Unidentified
PN JP 1999116599-A/4
PD 27-APR-1999
PF 14-OCT-1997 JP 1997280831
PR
PI SHIGEHIRO IKEDA, KENJI YAMAMOTO
PC C07K14/52, C07K16/28, C12N15/09, C12Q1/68//C12P21/02, (C12P21/02,
C12R1/19),
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FT Key
Location/Qualifiers
1..28
source
/organism="Unidentified".
FEATURES
Location/Qualifiers
1..28
source
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
7 t
BASE COUNT
8 a 8 c 5 g
ORIGIN
Query Match
Best Local Similarity 11.7%; Score 16.2; DB 6; Length 28;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 62 CAGCGTGGTGGAGTTGGTT 82
DB 25 CAGCGTGGTGGAGTTGAATT 5
RESULT 9
AX597968
LOCUS
DEFINITION
Sequence 242 from Patent WO0244994.
ACCESSION
AX597968
VERSION
AX597968.1 GI:28398141
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
AUTHORS
Brower, A., Brow, M. A., Cracauer, R. F., Fors, L., Granske, R., de arruda
Indig, M., Kurensky, D., Luedtke, C., Lukowiak, A. A., Lyamichev, V.,
Neri, B. P., Reimer, N. D., Roeven, R. T., Skrzypczynski, Z., Ziarno, W. A.,
Comerford, J., Stump, S. and Viegut, D. D.
TITLE
Systems and method for detection assay production and sale
JOURNAL
Patent: WO 0244994-A 242 06-JUN-2002;
FEATURES
Location/Qualifiers
1..29
source
/organism="synthetic construct"
/mol_type="genomic DNA"
```

```

BASE COUNT      5 a      5 c      12 g      6 t      1 others
ORIGIN

Query Match
Best Local Similarity 11.7%; Score 16.2; DB 6; Length 29;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 98 GAGATTCGGTCCCAACTCCTC 118
Db 27 GAATTCCTCCCAACTCCTC 7

RESULT 10
LOCUS AR018179/c
DEFINITION Sequence 6 from patent US 5780611.
ACCESSION AR018179
VERSION AR018179.1 GI:3973782
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 30)
AUTHORS Guntaka,R.V.; Weber,K.Theodore.; Kovacs,A. and Kandala,J.
TITLE Oligomers which inhibit expression of collagen genes
JOURNAL Patent: US 5780611-A 6 14-JUL-1998;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
BASE COUNT 11 a 0 c 19 g 0 t
ORIGIN

Query Match
Best Local Similarity 11.7%; Score 16.2; DB 6; Length 30;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 106 CTCCCAACTCCTCCCTATCCT 126
Db 30 CTCCCTCCCTCCCTCTCCT 10

RESULT 11
LOCUS AX180867/c
DEFINITION Sequence 15 from Patent WO0146691.
ACCESSION AX180867
VERSION AX180867.1 GI:15132696
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Joly,B.
TITLE A bioluminescence resonance energy transfer (bret) system with
broad spectral resolution between donor and acceptor emission
wavelengths and its use
JOURNAL Patent: WO 0146691-A 15 28-JUN-2001;
BioSignal Packard Inc. (CA)
FEATURES Location/Qualifiers
source 1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT 7 a 9 c 12 g 2 t
ORIGIN

Query Match
Best Local Similarity 11.7%; Score 16.2; DB 6; Length 30;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 47 CCCTGGTGTCTCTCCAGCGTGGAAG 75

```

```

Db 30 CCCGGTTCTCCCCCATGGTGGCGCTAG 2

RESULT 12
LOCUS E28689
DEFINITION Primer for detecting hepatitis B virus and method for detecting
hepatitis B virus therewith.
ACCESSION E28689
VERSION E28689.1 GI:13020850
KEYWORDS JP 1999262399-A/22.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 25)
AUTHORS Masakazu,M., Shuichi,K. and Kazumasa,H.
TITLE Primer for detecting hepatitis B virus and method for detecting
hepatitis B virus therewith
JOURNAL Patent: JP 1999262399-A 22 28-SEP-1999;
SRL-INC
COMMENT OS Unidentified
PN JP 1999262399-A/22
PD 28-SEP-1999
PF 17-MAR-1998 JP 1998087977
PR MASAKAZU MUKAIDE, SHUICHI KANEKO, KAZUMASA HIKIJI PC
C12Q1/68, C07K14/02, C12Q1/70//C12N15/09, C12N15/00 CC Strandedness:
Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..25
/organism="Unidentified"
FEATURES Location/Qualifiers
source 1..25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 1 a 7 c 6 g 9 t 2 others
ORIGIN

Query Match
Best Local Similarity 11.5%; Score 16; DB 6; Length 25;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 42 TGGAACCTCGTCTCCTCCTC 61
Db 5 TGGACCTTGTGKCTCCTC 24

RESULT 13
LOCUS A64642
DEFINITION Sequence 8 from Patent WO9731111.
ACCESSION A64642
VERSION A64642.1 GI:4530738
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Oude,E.R., Paulusma,C.C., Bosma,P.J., Borst,P., Evers,R., Kool and
Marcel.
TITLE A FAMILY OF ORGANIC ANION TRANSPORTERS, NUCLEIC ACIDS ENCODING
THEM, CELLS COMPRISING THEM AND METHODS FOR USING THEM
JOURNAL Patent: WO 9731111-A 8 28-AUG-1997;
INTROGENE BV (NL)
COMMENT Other publication AU 1736697 19970910.
FEATURES Location/Qualifiers
source 1..26
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

```

BASE COUNT 4 a 9 c 6 g 7 t

Query Match 11.5%; Score 16; DB 6; Length 26;
Best Local Similarity 79.2%; Pred. No. 4.8e+06;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 29 CCAGGCTCAGCTGGAACCTGG 52
|||||
Db 2 CCAGGTTACATCTCGACTCTGG 25
|||||

RESULT 14
AR009754/c
LOCUS AR009754 30 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 7 from patent US 5756448.
ACCESSION AR009754
VERSION AR009754.1 GI:3968559
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Moore, D.D. and Baes, M.I.
TITLE Constitutive activator of retinoid (CAR) receptor polypeptides
JOURNAL Patent: US 5756448-A 7 26-MAY-1998;
FEATURES Location/Qualifiers
1..30
source

BASE COUNT 8 a 7 c 12 g 3 t

Query Match 11.2%; Score 15.6; DB 6; Length 30;
Best Local Similarity 70.0%; Pred. No. 6.3e+06;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 35 TCACAGCTGGAACCTGGTCTCTCCAG 64
|||||
Db 30 TCAGGCTGCTCTCTCTCTCTCTCTCCAG 1
|||||

RESULT 15
I73485/c
LOCUS I73485 30 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 7 from patent US 5686574.
ACCESSION I73485
VERSION I73485.1 GI:3009626
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Moore, D.D. and Baes, M.I.
TITLE Constitutive activator of retinoid acid response (car) receptor fusion protein
JOURNAL Patent: US 5686574-A 7 11-NOV-1997;
FEATURES Location/Qualifiers
1..30
source

BASE COUNT 8 a 7 c 12 g 3 t

Query Match 11.2%; Score 15.6; DB 6; Length 30;
Best Local Similarity 70.0%; Pred. No. 6.3e+06;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 35 TCACAGCTGGAACCTGGTCTCTCCAG 64
|||||
Db 30 TCAGGCTGCTCTCTCTCTCTCTCTCCAG 1
|||||

RESULT 16
I84194/c

LOCUS I81194 30 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 7 from patent US 5710017.
ACCESSION I81194
VERSION I81194.1 GI:3209484
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Moore, D.D. and Baes, M.I.
TITLE DNA encoding a constitutive activator retinoic acid response (CAR) receptor
JOURNAL Patent: US 5710017-A 7 20-JAN-1998;
FEATURES Location/Qualifiers
1..30
source

BASE COUNT 8 a 7 c 12 g 3 t

Query Match 11.2%; Score 15.6; DB 6; Length 30;
Best Local Similarity 70.0%; Pred. No. 6.3e+06;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 35 TCACAGCTGGAACCTGGTCTCTCCAG 64
|||||
Db 30 TCAGGCTGCTCTCTCTCTCTCTCTCCAG 1
|||||

RESULT 17
AX081599
LOCUS AX081599 25 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 104 from Patent WO0109350.
ACCESSION AX081599
VERSION AX081599.1 GI:13170424
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Berthet, P.X., Dalemans, W.L., Denoel, P., Dequesne, G.S., Feron, C.S., Lobet, Y.S., Poolman, J.S., Thiry, G.S., Lhonnard, J.S. and Voet, P.S.
TITLE Genetically engineered bleb vaccine
JOURNAL Patent: WO 0109350-A 104 08-FEB-2001;
FEATURES SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)
Location/Qualifiers
1..25
source

BASE COUNT 6 a 12 c 2 g 5 t

Query Match 11.1%; Score 15.4; DB 6; Length 25;
Best Local Similarity 76.0%; Pred. No. 7.5e+06;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 109 CCAACTCTCTCTATCTCTAAAGCC 133
|||||
Db 1 CCAATCTCTCTCTCTCTCTCTAAAGCC 25
|||||

RESULT 18
AX374780
LOCUS AX374780 25 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 104 from Patent WO0209746.
ACCESSION AX374780
VERSION AX374780.1 GI:19169682
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.

12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 84

```

KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 30)
Albrecht,G., Brenner,S. and Dubridge,R.B.
TITLE
Solid phase screening of differentially expressed genes
JOURNAL
Patent: US 651802-A 24 28-JAN-2003;
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"
BASE COUNT      5 a      8 c      7 g      7 t      3 others
ORIGIN
Query Match      10.9%; Score 15.2; DB 6; Length 30;
Best Local Similarity 85.0%; Pred. No. 8.4e+06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      37 ACAGCTGGAACCCCTGGTGTC 56
      ||||| ||||| ||||| ||||| |||||
Db      6 ACAGCTGCATCCCTGGTGAC 25

RESULT 23
AR279994
LOCUS      AR279994      30 bp      DNA      linear      PAT 10-APR-2003
DEFINITION      Sequence 26 from patent US 6518023.
ACCESSION      AR279994
VERSION      AR279994.1 GI:29715183
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 30)
Brenner,S.
TITLE
Method of mapping restriction sites in polynucleotides
JOURNAL
Patent: US 6518023-A 26 11-FEB-2003;
FEATURES
source
Location/Qualifiers
1..30
/organism="unknown"
BASE COUNT      5 a      8 c      7 g      7 t      3 others
ORIGIN
Query Match      10.9%; Score 15.2; DB 6; Length 30;
Best Local Similarity 85.0%; Pred. No. 8.4e+06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      37 ACAGCTGGAACCCCTGGTGTC 56
      ||||| ||||| ||||| ||||| |||||
Db      6 ACAGCTGCATCCCTGGTGAC 25

RESULT 24
BD128452
LOCUS      BD128452      30 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION      Solid phase screening of differentially expressed genes.
ACCESSION      BD128452
VERSION      BD128452.1 GI:23223397
KEYWORDS      JP 2002500050-A/24.
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 30)
Albrecht,G., Brenner,S. and Dubridge,R.
AUTHORS
Solid phase screening of differentially expressed genes
TITLE
Patent: JP 2002500050-A 24 08-JAN-2002;
JOURNAL
LYNX THERAPEUTICS INC
COMMENT
OS Artificial Sequence
PN JP 2002500050-A/24
PD 08-JAN-2002
PF 08-JAN-1999 JP 2000527674
PR 09-JAN-1998 US 09/005222,06-AUG-1998 US 09/130446 PI
GLENN ALBRECHT, SYDNEY BRENNER, ROBERT DUBRIDGE PC

C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Synthetic CC n can be a
or g or c or t
CC n can be a or g or c or t
FH Key Location/Qualifiers
FT misc difference (1)..(2)
FT misc difference (4).
Location/Qualifiers
1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT      5 a      8 c      7 g      7 t      3 others
ORIGIN
Query Match      10.9%; Score 15.2; DB 6; Length 30;
Best Local Similarity 85.0%; Pred. No. 8.4e+06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      37 ACAGCTGGAACCCCTGGTGTC 56
      ||||| ||||| ||||| ||||| |||||
Db      6 ACAGCTGCATCCCTGGTGAC 25

RESULT 25
BD133164
LOCUS      BD133164      30 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION      Method of mapping restriction sites in polynucleotides.
ACCESSION      BD133164
VERSION      BD133164.1 GI:23228109
KEYWORDS      JP 2002507126-A/26.
SOURCE
ORGANISM
Arabidopsis sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1 (bases 1 to 30)
Brenner,S.
AUTHORS
Method of mapping restriction sites in polynucleotides
TITLE
Patent: JP 2002507126-A 26 05-MAR-2002;
JOURNAL
LYNX THERAPEUTICS INC
COMMENT
PN JP 2002507126-A/26
PD 05-MAR-2002
PF 25-JUN-1998 JP 1999505776
PR 27-JUN-1997 US 08/884189
PI SYDNEY BRENNER
PC C12Q1/68
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
1..30
/organism="Arabidopsis sp."
/mol_type="genomic DNA"
/db_xref="taxon:29726"
BASE COUNT      5 a      8 c      7 g      7 t      3 others
ORIGIN
Query Match      10.9%; Score 15.2; DB 6; Length 30;
Best Local Similarity 85.0%; Pred. No. 8.4e+06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      37 ACAGCTGGAACCCCTGGTGTC 56
      ||||| ||||| ||||| ||||| |||||
Db      6 ACAGCTGCATCCCTGGTGAC 25

Search completed: August 22, 2003, 10:37:12
Job time : 1668 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 08:41:19 ; Search time 170 Seconds
(without alignments)

Title: US-09-925-139-3_COPY_1631_1769
Perfect score: 139
Sequence: 1 ggatgggggttagcagaa.....ctatcctaaggccactgg 139

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2101872

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_19Jun03.*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	21	15.1	21	22	AAI6686
C 2	20	14.4	20	24	AAI6686
C 3	20	14.4	20	25	ABX13031
C 4	20	14.4	20	25	ABX12175
C 5	20	14.4	20	25	ABX12198
C 6	20	14.4	20	25	ABX12199
C 7	20	14.4	20	25	ABX12200
C 8	20	14.4	20	25	ABX12217
C 9	20	14.4	20	25	ABX12218
C 10	20	14.4	20	25	ABX12219
C 11	20	14.4	20	25	ABX12220
C 12	20	14.4	20	25	ABX12221
C 13	20	14.4	20	25	ABX12222
C 14	20	14.4	20	25	ABX12223
C 15	20	14.4	20	25	ABX12224
C 16	20	14.4	20	25	ABX12225
C 17	20	14.4	20	25	ABX12226
C 18	20	14.4	20	25	ABX12227
C 19	20	14.4	20	25	ABX12228
C 20	20	14.4	20	25	ABX12229
C 21	20	14.4	20	25	ABX12230
C 22	20	14.4	20	25	ABX12231
C 23	20	14.4	20	25	ABX12232
C 24	20	14.4	20	25	ABX12233
C 25	20	14.4	20	25	ABX12234
C 26	20	14.4	20	25	ABX12235
C 27	20	14.4	20	25	ABX12236
C 28	20	14.4	20	25	ABX12237
C 29	20	14.4	20	25	ABX12238
C 30	20	14.4	20	25	ABX12239
C 31	20	14.4	20	25	ABX12240
C 32	20	14.4	20	25	ABX12241
C 33	20	14.4	20	25	ABX12242
C 34	20	14.4	20	25	ABX12243
C 35	20	14.4	20	25	ABX12244
C 36	20	14.4	20	25	ABX12245
C 37	20	14.4	20	25	ABX12246
C 38	20	14.4	20	25	ABX12247
C 39	20	14.4	20	25	ABX12248
C 40	20	14.4	20	25	ABX12249
C 41	20	14.4	20	25	ABX12250
C 42	20	14.4	20	25	ABX12251
C 43	20	14.4	20	25	ABX12252
C 44	20	14.4	20	25	ABX12253
C 45	20	14.4	20	25	ABX12254
C 46	20	14.4	20	25	ABX12255
C 47	20	14.4	20	25	ABX12256
C 48	20	14.4	20	25	ABX12257
C 49	20	14.4	20	25	ABX12258
C 50	20	14.4	20	25	ABX12259
C 51	20	14.4	20	25	ABX12260
C 52	20	14.4	20	25	ABX12261
C 53	20	14.4	20	25	ABX12262
C 54	20	14.4	20	25	ABX12263
C 55	20	14.4	20	25	ABX12264
C 56	20	14.4	20	25	ABX12265
C 57	20	14.4	20	25	ABX12266
C 58	20	14.4	20	25	ABX12267
C 59	20	14.4	20	25	ABX12268
C 60	20	14.4	20	25	ABX12269
C 61	20	14.4	20	25	ABX12270
C 62	20	14.4	20	25	ABX12271
C 63	20	14.4	20	25	ABX12272
C 64	20	14.4	20	25	ABX12273
C 65	20	14.4	20	25	ABX12274
C 66	20	14.4	20	25	ABX12275
C 67	20	14.4	20	25	ABX12276
C 68	20	14.4	20	25	ABX12277
C 69	20	14.4	20	25	ABX12278
C 70	20	14.4	20	25	ABX12279
C 71	20	14.4	20	25	ABX12280
C 72	20	14.4	20	25	ABX12281
C 73	20	14.4	20	25	ABX12282
C 74	20	14.4	20	25	ABX12283
C 75	20	14.4	20	25	ABX12284
C 76	20	14.4	20	25	ABX12285
C 77	20	14.4	20	25	ABX12286
C 78	20	14.4	20	25	ABX12287
C 79	20	14.4	20	25	ABX12288
C 80	20	14.4	20	25	ABX12289
C 81	20	14.4	20	25	ABX12290

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

Human cholesterol

C 82	15	10.8	30	16	AAQ89012	VEGF 2'-NH2-RNA nu
C 83	14.8	10.6	20	24	ABSG0987	Human genotyping P
C 84	14.8	10.6	24	22	AAH28671	Human interleukin-6
C 85	14.8	10.6	25	22	AAH16197	Soybean 2400L7 reg
C 86	14.8	10.6	26	22	AAH78617	PCR primer Ex2Dn(2)
C 87	14.8	10.6	27	16	AAH04690	Black widow spider
C 88	14.8	10.6	27	24	AAK99801	Bacillus sp alkali
C 89	14.8	10.6	30	15	AAQ67087	CHC-2 primer. Syn
C 90	14.8	10.6	30	21	AAZ88251	Treponea pallidum
C 91	14.8	10.6	30	22	AAH60081	Primer #5 for gene
C 92	14.6	10.5	21	21	AAH36969	Human dysferlin ex
C 93	14.6	10.5	21	21	AAH11514	Human dysferlin ex
C 94	14.6	10.5	24	22	AAH45241	Human rhoc PCR pri
C 95	14.6	10.5	24	24	AAH50713	Pseudomonas glutar
C 96	14.6	10.5	24	24	AAH18863	Growth hormone 1 g
C 97	14.6	10.5	24	24	ABH89890	Capture oligonucle
C 98	14.6	10.5	24	24	ABH89891	Capture oligonucle
C 99	14.6	10.5	25	24	ABV92964	Human POSHL1 scann
C 100	14.6	10.5	25	24	ABV92965	Human POSHL1 scann
C 101	14.6	10.5	27	24	AAU50701	Pseudomonas glutar
C 102	14.6	10.5	29	18	AAH45117	Cytomegalovirus po
C 103	14.6	10.5	29	18	AAH45117	Polyomorphi fragme
C 104	14.6	10.5	30	17	AAH41675	Endo-xyloglucan tr
C 105	14.6	10.5	30	20	AAH23514	T cell receptor V
C 106	14.6	10.5	30	24	ABK15255	Hepatitis B virus
C 107	14.4	10.4	18	24	ABU58444	CYP-C probe genera
C 108	14.4	10.4	20	24	ABZ31506	Candida albicans G
C 109	14.4	10.4	20	24	ABV73609	S. albulus plasmid
C 110	14.4	10.4	20	24	ABH93783	Capture oligonucle
C 111	14.4	10.4	21	24	ABQ93591	Human DISC1/DIS2
C 112	14.4	10.4	24	20	AAZ40497	Degenerate primer
C 113	14.4	10.4	24	21	AAH08873	5' RACE primer for
C 114	14.4	10.4	24	21	AAH08873	Nested 3' RACE pri
C 115	14.4	10.4	24	22	AAH08718	Forward PCR primer
C 116	14.4	10.4	24	22	AAH04190	A. niger LLP-2 C-
C 117	14.4	10.4	24	24	ABQ00835	Oligonucleotide ad
C 118	14.4	10.4	24	24	ABQ05632	Oligonucleotide ad
C 119	14.4	10.4	24	24	ABQ05673	Oligonucleotide ad
C 120	14.4	10.4	24	24	ABH84136	Capture oligonucle
C 121	14.4	10.4	24	24	ABH84137	Capture oligonucle
C 122	14.4	10.4	25	21	AAH37218	Human PR01279 reve
C 123	14.4	10.4	25	22	AAH54325	Primer #48 used in
C 124	14.4	10.4	25	24	AAH11088	Small acid-soluble
C 125	14.4	10.4	25	24	ABN11290	Human GDMPLP-1 25-m
C 126	14.4	10.4	25	24	ABN11291	Primer used when o
C 127	14.4	10.4	26	18	AAV06178	Primer 1 for human
C 128	14.4	10.4	26	21	AAH47218	Human PDE10A 5' RA
C 129	14.4	10.4	26	22	ABQ03666	Human genomic DNA
C 130	14.4	10.4	26	24	ABQ39292	Human gene specifi
C 131	14.4	10.4	26	24	ABK65554	Human gene specifi
C 132	14.4	10.4	26	24	ABK65562	Bacillus sp. pecti
C 133	14.4	10.4	27	19	AAV59485	Bacillus sp. pecti
C 134	14.4	10.4	27	22	AAH22440	P450RAI-2 polypt
C 135	14.4	10.4	27	24	ABQ74191	Human cytochrome P
C 136	14.4	10.4	27	24	ABQ74191	Primer for DNA enc
C 137	14.4	10.4	28	22	AAH77658	Sense PCR primer i
C 138	14.4	10.4	28	22	AAH45591	Phagemid vector pc
C 139	14.4	10.4	28	22	AAH45591	Oligonucleotide #1
C 140	14.4	10.4	28	22	AAH45591	Rat secreted facto
C 141	14.4	10.4	28	24	AAH54738	Blocking oligonucle
C 142	14.4	10.4	29	25	ABV76930	HBV amplifier prob
C 143	14.4	10.4	30	14	AAQ45815	PCR primer for HSV
C 144	14.4	10.4	30	15	AAQ73656	FC receptor PCR pr
C 145	14.4	10.4	30	16	AAQ86854	Herbicide-resistan
C 146	14.4	10.4	30	18	AAH27377	Ovine IL-12 35 kd
C 147	14.4	10.4	30	18	AAH27377	Chimeric FcgammaRI
C 148	14.4	10.4	30	19	AAV56028	Chimeric FcgammaRI
C 149	14.4	10.4	30	19	AAV56029	HBV.84 amplifier p
C 150	14.4	10.4	30	19	AAV07812	Amplifier probe HB
C 151	14.4	10.4	30	20	AAV83041	HSV-2 gH gene PCR
C 152	14.4	10.4	30	20	AAV64106	Human FC receptor
C 153	14.4	10.4	30	21	AAH60012	PCR primer 1b for
C 154	14.4	10.4	30	25	ABX15171	
C 155	14.4	10.4	30	25	ABX15172	PCR primer 2a for
C 156	14.2	10.2	20	16	AAH08224	Hepatitis B virus
C 157	14.2	10.2	20	16	AAQ81567	Europium (III) tex
C 158	14.2	10.2	20	16	AAQ80879	Europium (III) tex
C 159	14.2	10.2	20	16	AAQ80880	Dysprosium (III) t
C 160	14.2	10.2	20	16	AAQ91455	Oligonucleotide #4
C 161	14.2	10.2	20	19	AAV07290	Texaphyrin oligonu
C 162	14.2	10.2	20	19	AAV07037	Antisense primer f
C 163	14.2	10.2	20	20	AAV99212	Exemplary texaphyr
C 164	14.2	10.2	20	21	AAZ88439	Human diacylglycer
C 165	14.2	10.2	20	22	AAAD05958	Human RECOL2 antis
C 166	14.2	10.2	20	24	AAAD1746	Stabilising reagen
C 167	14.2	10.2	20	25	ABT23628	HPV-16, synthetic
C 168	14.2	10.2	22	24	ABK14592	mRNA target probe.
C 169	14.2	10.2	22	24	ABK14592	Probe for the den
C 170	14.2	10.2	25	15	AAQ55871	Probe used for det
C 171	14.2	10.2	25	16	AAQ55871	Goose malonyl CoA
C 172	14.2	10.2	26	21	AAZ87691	ICE-LAP-1 5' PCR p
C 173	14.2	10.2	27	17	AAH15580	Human BUB1B kinase
C 174	14.2	10.2	27	20	AAH58976	Human synaptotomal
C 175	14.2	10.2	27	20	AAH58976	PCR primer PDM-208
C 176	14.2	10.2	27	20	AAH58976	Human SCP-1 RT-PCR
C 177	14.2	10.2	27	22	AAH38915	Human SCP-1 RT-PCR
C 178	14.2	10.2	27	22	AAH38915	SNP specific SNPE
C 179	14.2	10.2	27	22	AAH38915	SNP specific SNPE
C 180	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 181	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 182	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 183	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 184	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 185	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 186	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 187	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 188	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 189	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 190	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 191	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 192	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 193	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 194	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 195	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 196	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 197	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 198	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 199	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 200	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 201	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 202	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 203	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 204	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 205	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 206	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 207	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 208	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 209	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 210	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 211	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 212	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 213	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 214	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 215	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 216	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 217	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 218	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 219	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 220	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 221	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 222	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 223	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 224	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 225	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 226	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR
C 227	14.2	10.2	27	22	AAH38915	Human CTAGE-1 PCR

C 228	14	10.1	27	19	AAV96837	Potato citrate syn	301	13.6	9.8	20	14	AAQ46059	Sequence of PCR pr
C 229	14	10.1	29	21	AAQ4493	Polymorphic fragme	302	13.6	9.8	20	17	AAT42248	Primer derived fro
C 230	14	10.1	30	16	AAQ87759	Human auxillary cy	303	13.6	9.8	20	18	AAT66085	Plasmidogen activa
C 231	14	10.1	30	17	AAT48337	Primer for 0.9 kb	304	13.6	9.8	20	19	AAV62008	L monocytogenes hl
C 232	14	10.1	30	17	AAT26949	Human cytochrome p	C 305	13.6	9.8	20	20	AAZ04070	PCR primer used to
C 233	14	10.1	30	22	AAI67228	Lipophilin B speci	C 306	13.6	9.8	20	20	AAZ07388	Primer used to amp
C 234	14	10.1	30	24	ABX68376	Novel Helicobacter	C 307	13.6	9.8	20	20	AAZ97331	Primer used to amp
C 235	14	10.1	30	24	AD351573	Human UGT1A9 gene	308	13.6	9.8	20	20	AAZ78426	Rat GAPDH primer 3
C 236	14	10.1	30	24	ABK51803	Human amphipysin-	309	13.6	9.8	20	20	AAZ59299	GAPDH reverse prim
C 237	14	10.1	30	24	AD334986	Human SDF1 gene si	C 310	13.6	9.8	20	20	AAZ22801	PCR primer 82689
C 238	14	10.1	30	24	AAZ34987	Human SDF1 gene si	C 311	13.6	9.8	20	20	AAZ76046	Human biallelic ma
C 239	14	10.1	30	24	AD335001	SDF1 mismatched ol	C 312	13.6	9.8	20	22	AAH80623	Oligonucleotide hy
C 240	14	10.1	30	24	ABL51601	Oligonucleotide SG	C 313	13.6	9.8	20	22	AAH20719	SNP specific lower
C 241	14	10.1	30	25	AD53642	PCR primer #1 used	C 314	13.6	9.8	20	22	AAH38150	Glycerolaldehyde-3-p
C 242	14	10.1	30	25	ABV77470	P. monodon mature	C 315	13.6	9.8	20	22	AAH20719	Glycerolaldehyde-3-p
C 243	13.8	9.9	17	20	AAV91005	Human C-raf target	C 316	13.6	9.8	20	24	ABN83384	Human Class I HLA-
C 244	13.8	9.9	17	20	AAV91006	Human C-raf target	C 317	13.6	9.8	20	24	ABN83384	Locus specific amp
C 245	13.8	9.9	18	20	AAZ28045	PCR primer for hum	C 318	13.6	9.8	20	25	ABN83384	Human gene single
C 246	13.8	9.9	20	19	AAV26436	PCR primer "A" gamm	C 319	13.6	9.8	21	21	AAV02712	Human ADN oligonuc
C 247	13.8	9.9	20	21	AAV65593	Human tetra-6-desa	C 320	13.6	9.8	21	21	AAZ61424	Human WMP-20 PCR p
C 248	13.8	9.9	20	22	AAH19416	Human uteroglobin	C 321	13.6	9.8	21	22	AAZ61424	Rat hepatocyte car
C 249	13.8	9.9	20	22	AAH78641	Probe for mechan	C 322	13.6	9.8	21	22	AAZ61424	Mutagenic primer u
C 250	13.8	9.9	20	24	AD22845	CD34 cell marker D	C 323	13.6	9.8	21	25	ABT13358	Vector pVAC1 const
C 251	13.8	9.9	20	25	ABX78257	Human bifunctional	C 324	13.6	9.8	22	21	AAH87626	Primer to amplify
C 252	13.8	9.9	20	25	ABX10328	Coryneform bacteri	C 325	13.6	9.8	22	21	AAH87626	MCSP PCR primer p3
C 253	13.8	9.9	21	21	AAA94234	Human testosterone	C 326	13.6	9.8	23	15	AAQ62402	Candida albicans G
C 254	13.8	9.9	22	24	ABX97402	Human NOV-associat	C 327	13.6	9.8	23	15	AAQ62402	Fas antigen relate
C 255	13.8	9.9	22	24	ABX97402	Human multidrug re	C 328	13.6	9.8	23	15	AAQ62402	Homo sapiens PSPL
C 256	13.8	9.9	24	22	ABX66707	Human ribosomal pr	C 329	13.6	9.8	23	18	AAT60464	Human peroxisome
C 257	13.8	9.9	25	12	AAI69892	Primer/probe 038 f	C 330	13.6	9.8	23	24	ABN85359	EBEC human pathoge
C 258	13.8	9.9	25	24	AAH42718	A promoter element	C 331	13.6	9.8	24	19	AAV29529	Oligonucleotide ad
C 259	13.8	9.9	25	24	ABV92959	Human POSHL1 scann	C 332	13.6	9.8	24	22	AAH45824	Oligonucleotide ad
C 260	13.8	9.9	25	24	ABQ12170	Oligonucleotide ad	C 333	13.6	9.8	24	22	AAH45824	Oligonucleotide ad
C 261	13.8	9.9	25	24	ABN11292	Human GDMPL-1 25-m	C 334	13.6	9.8	24	24	ABQ03230	Oligonucleotide ad
C 262	13.8	9.9	26	22	AAZ74324	Human H11 coding s	C 335	13.6	9.8	24	24	ABQ03230	Oligonucleotide ad
C 263	13.8	9.9	26	22	AAZ83676	Human b actin anti	C 336	13.6	9.8	24	24	ABQ03230	Oligonucleotide ad
C 264	13.8	9.9	26	24	AAZ47351	Human neurotrophide	C 337	13.6	9.8	24	24	ABQ03230	Oligonucleotide ad
C 265	13.8	9.9	26	25	ABX77379	Human h439 PCR pr	C 338	13.6	9.8	24	24	ABQ03230	Oligonucleotide ad
C 266	13.8	9.9	27	13	AAQ24565	NANBH peptide B pr	C 339	13.6	9.8	24	25	ABZ57977	Human clathrin lig
C 267	13.8	9.9	27	14	AAQ47315	PCR primer for mit	C 340	13.6	9.8	25	15	ABZ57977	PR-10a silencing e
C 268	13.8	9.9	27	14	AAQ51484	Dengue virus seque	C 341	13.6	9.8	25	16	AAQ88752	HIV-1 pol3 primer.
C 269	13.8	9.9	27	14	AAQ51484	Platelet mitochond	C 342	13.6	9.8	25	16	AAQ88752	PCR detection prim
C 270	13.8	9.9	27	18	AAV06612	G-protein coupled	C 343	13.6	9.8	25	20	AAZ22330	HIV-1 PCR primer p
C 271	13.8	9.9	27	18	AAV06612	Hyaluronic acid re	C 344	13.6	9.8	25	24	ABV92966	Human POSHL1 scann
C 272	13.8	9.9	27	24	ABG61024	Human automated ge	C 345	13.6	9.8	25	25	ABQ13165	Oligonucleotide ad
C 273	13.8	9.9	27	24	ABG61024	Human SPHK1 CDNA c	C 346	13.6	9.8	25	25	ABQ13165	Oligonucleotide ad
C 274	13.8	9.9	28	19	AAV62695	Phenolic acid este	C 347	13.6	9.8	26	21	AAZ96559	Human DPP10 Tagman
C 275	13.8	9.9	28	21	AAZ12385	PCR primer SEQ ID	C 348	13.6	9.8	26	21	AAZ96559	Reverse PCR primer
C 276	13.8	9.9	28	21	AAZ12385	Human PRV-1 PCR pr	C 349	13.6	9.8	26	21	AAZ96559	Internal positive
C 277	13.8	9.9	28	25	AAZ53946	Human PRV-1 antis	C 350	13.6	9.8	26	22	AAH46473	PCR primer iPC-R1
C 278	13.8	9.9	29	14	AAQ40501	Oligo #34 used to	C 351	13.6	9.8	26	22	AAH46473	Reverse PCR primer
C 279	13.8	9.9	29	15	AAQ77888	ALT primer-2... Syn	C 352	13.6	9.8	26	22	AAH46473	Human CFTR exon 18
C 280	13.8	9.9	29	18	AAZ73506	Neural thread prot	C 353	13.6	9.8	27	15	AAQ94652	PCR primer #4. Un
C 281	13.8	9.9	29	18	AAZ73506	Human macrophage m	C 354	13.6	9.8	27	17	AAQ94652	Recombinant cold-r
C 282	13.8	9.9	29	19	AAV31143	p85 PCR primer SEQ	C 355	13.6	9.8	27	21	AAZ74828	Primer 3, amplifie
C 283	13.8	9.9	29	19	AAV20993	PCR primer for ALC	C 356	13.6	9.8	27	21	AAZ74828	Human IFN-alpha2 m
C 284	13.8	9.9	29	20	AAZ57853	PCR primer used in	C 357	13.6	9.8	27	22	AAH43009	Human IFN-alpha2 m
C 285	13.8	9.9	29	21	AAZ57853	Recombination effi	C 358	13.6	9.8	27	22	AAH43009	PCR primer for mur
C 286	13.8	9.9	29	22	AAZ57853	PCR primer attB2.5	C 359	13.6	9.8	28	19	AAV12066	Murine Iad beta ch
C 287	13.8	9.9	29	22	AAH40785	SNP specific upper	C 360	13.6	9.8	28	21	AAZ94107	Fruit-associated b
C 288	13.8	9.9	29	22	AAH40785	Primer 32359 for c	C 361	13.6	9.8	28	22	AAZ94107	P. syringae pv. to
C 289	13.8	9.9	29	24	AAZ82093	Brevibacterium fla	C 362	13.6	9.8	28	24	AAZ94107	Influenza A/Udorn/
C 290	13.8	9.9	29	24	ABK15061	B. napus ILPRBn ge	C 363	13.6	9.8	29	21	AAZ94107	Bovine beta-casein
C 291	13.8	9.9	29	24	ABK15061	nef coding region	C 364	13.6	9.8	29	21	AAZ94107	Contig 2535-based
C 292	13.8	9.9	30	13	AAQ35855	PCR primer PNEFBAM	C 365	13.6	9.8	29	21	AAZ94107	PCR primer PDM-229
C 293	13.8	9.9	30	14	AAQ35855	Oligonucleotide 11	C 366	13.6	9.8	29	24	ABZ71846	Human delta5-desat
C 294	13.8	9.9	30	18	AAZ65531	c-mpl receptor ago	C 367	13.6	9.8	29	24	ABZ71846	Ehrlichia antigen
C 295	13.8	9.9	30	18	AAZ65531	Primer 116-3' for	C 368	13.6	9.8	29	24	ABZ71846	Human granulocyte
C 296	13.8	9.9	30	19	AAV55443	Dendritic cell-der	C 369	13.6	9.8	30	15	AAQ67086	CHC-1 primer. Syn
C 297	13.8	9.9	30	19	AAV33074	CD44 V3C-RP-BamH1	C 370	13.6	9.8	30	16	AAQ67086	Nitrocellulose-bln
C 298	13.8	9.9	30	20	AAZ06330	PCR primer PH784 u	C 371	13.6	9.8	30	17	AAZ06330	Human genomic DNA
C 299	13.8	9.9	30	22	AAZ06330	Primer used for hu	C 372	13.6	9.8	30	20	AAZ06330	Gluconobacter oxyd
C 300	13.8	9.9	30	22	AAZ06330		C 373	13.6	9.8	30	21	AAZ06330	

C 520	13.2	9.5	20	24	ABL94348	Mouse C/EBP beta p	C 593	13.2	9.5	26	25	ABX81167	Human secreted or
C 521	13.2	9.5	20	25	ABZ37372	Kappa light chain	C 594	13.2	9.5	26	25	ABX90257	Human secreted/tra
C 522	13.2	9.5	21	16	AAZ04956	Upstream primer fo	C 595	13.2	9.5	26	25	ABX77868	Human PRO PCR prim
C 523	13.2	9.5	21	19	AAZ28664	Human polymorphic	C 596	13.2	9.5	26	25	ABX79464	Human secreted/tr
C 524	13.2	9.5	21	19	AAV33397	PCR primer MABCR1R	C 597	13.2	9.5	26	25	ABX64103	Human PRO DNA PCR
C 525	13.2	9.5	21	21	AAZ73047	Human biallelic ma	C 598	13.2	9.5	26	25	ABX17067	Human PRO PCR prim
C 526	13.2	9.5	21	21	AAA72338	Human RecQ4 helica	C 599	13.2	9.5	27	18	AAZ89777	Plasmid pET-E2.123
C 527	13.2	9.5	21	21	AAZ92708	Rous sarcoma virus	C 600	13.2	9.5	27	18	AAZ88237	Primer EA21 for BP
C 528	13.2	9.5	21	22	AAZ96342	Human gene single	C 601	13.2	9.5	27	18	AAZ84579	Tat-E2 conjugate p
C 529	13.2	9.5	21	22	ABZ98164	Human multdrug re	C 602	13.2	9.5	27	19	AAZ98790	Human EGF-R hamme
C 530	13.2	9.5	21	24	ABZ98398	Human TIMP-1 promo	C 603	13.2	9.5	27	19	AAZ96930	Human EGF-R hamme
C 531	13.2	9.5	21	24	ABZ08425	Human Timp-1	C 604	13.2	9.5	27	19	AAZ96930	Potato citrate syn
C 532	13.2	9.5	21	24	ABK00112	Rous sarcoma virus	C 605	13.2	9.5	27	19	AAZ96930	TAT-E2 conjugate p
C 533	13.2	9.5	21	24	ABK98414	Mouse glyceraldehy	C 606	13.2	9.5	27	20	AAZ60284	PCR primer used to
C 534	13.2	9.5	21	25	ABK98975	Human AAGA SNP ana	C 607	13.2	9.5	27	20	AAZ57514	Presentin binding
C 535	13.2	9.5	22	18	AAZ85771	PMR2 gene PCR prim	C 608	13.2	9.5	27	22	AAZ63078	Shrimp white spot
C 536	13.2	9.5	22	19	AAZ21613	Human patched (ptc)	C 609	13.2	9.5	27	22	AAZ62282	PME-VPLF PCR prime
C 537	13.2	9.5	22	19	AAZ21613	Arabidopsis thalia	C 610	13.2	9.5	27	24	ABZ60998	Human genotyping p
C 538	13.2	9.5	22	22	AAZ26383	Arabidopsis riboso	C 611	13.2	9.5	27	24	ABZ60998	Human VPLF antibod
C 539	13.2	9.5	23	20	AAZ76539	Human WISP-3 PCR p	C 612	13.2	9.5	27	24	ABZ53799	BIAV S2 gene mutat
C 540	13.2	9.5	23	24	ABZ39565	Human cancer suppr	C 613	13.2	9.5	27	24	ABZ39520	Hepatitis C virus
C 541	13.2	9.5	24	14	AAQ09233	Probe Polalpha #23	C 614	13.2	9.5	27	24	ABZ26641	Bovine papillomavi
C 542	13.2	9.5	24	15	AAQ05800	Type II procollage	C 615	13.2	9.5	28	13	AAQ25474	HLA-A capture olig
C 543	13.2	9.5	24	20	AAZ57128	Human mutant KNO3	C 616	13.2	9.5	28	15	AAQ67014	Purine rich HER-2
C 544	13.2	9.5	24	20	AAZ18303	PCR primer for tel	C 617	13.2	9.5	28	15	AAQ70677	Endoglucanase type
C 545	13.2	9.5	24	22	AAZ16636	Gastric acid produ	C 618	13.2	9.5	28	19	AAZ44666	Purine rich region
C 546	13.2	9.5	24	22	AAZ16508	Human zinc finger	C 619	13.2	9.5	28	19	AAZ44666	Her-2/neu promoter
C 547	13.2	9.5	24	24	ABZ59345	Human hepsin/plasm	C 620	13.2	9.5	28	20	AAZ82714	Primer used in ana
C 548	13.2	9.5	24	24	ABQ00667	Oligonucleotide ad	C 621	13.2	9.5	28	20	AAZ82714	Partial sequence o
C 549	13.2	9.5	24	24	ABQ03263	Oligonucleotide ad	C 622	13.2	9.5	28	21	AAZ96604	PCR primer used to
C 550	13.2	9.5	24	24	ABQ03317	Oligonucleotide ad	C 623	13.2	9.5	28	21	AAZ96604	Xyloglucan endoglu
C 551	13.2	9.5	24	24	ABQ05301	Oligonucleotide ad	C 624	13.2	9.5	28	21	AAZ89549	Xyloglucan endoglu
C 552	13.2	9.5	24	24	ABQ05342	Oligonucleotide ad	C 625	13.2	9.5	28	22	AAZ02157	Partial DNA #7 enc
C 553	13.2	9.5	24	24	ABQ11588	Oligonucleotide ad	C 626	13.2	9.5	28	22	AAZ02157	Partial DNA #7 enc
C 554	13.2	9.5	24	24	ABQ11588	Oligonucleotide ad	C 627	13.2	9.5	28	22	AAZ82040	Xyloglucan endoglu
C 555	13.2	9.5	24	24	AAZ16174	HOMO DNA mismatch	C 628	13.2	9.5	28	22	AAZ82040	Partial nucleotide
C 556	13.2	9.5	25	19	AAZ30645	Telomerase reverse	C 629	13.2	9.5	28	22	AAZ77865	Partial XGU endogl
C 557	13.2	9.5	25	21	AAZ29639	Human apoptosis li	C 630	13.2	9.5	28	22	AAZ77865	Aspergillus aculea
C 558	13.2	9.5	25	22	AAZ37671	SNP specific SNPE	C 631	13.2	9.5	28	22	AAZ81158	Aspergillus aculea
C 559	13.2	9.5	25	22	AAZ39079	SNP specific SNPE	C 632	13.2	9.5	28	22	AAZ75779	Partial XGU endogl
C 560	13.2	9.5	25	24	ABV93312	Human POSHL1 scann	C 633	13.2	9.5	28	22	AAZ75756	Partial XGU endogl
C 561	13.2	9.5	25	24	ABV93313	Human POSHL1 scann	C 634	13.2	9.5	28	22	AAZ59738	A aculeatus xylogl
C 562	13.2	9.5	25	24	ABV93314	Human POSHL1 scann	C 635	13.2	9.5	28	22	AAZ89955	A aculeatus CBS 1
C 563	13.2	9.5	25	24	ABV93315	Human POSHL1 scann	C 636	13.2	9.5	29	13	AAZ29375	MHC-N, core of MHC
C 564	13.2	9.5	25	24	ABV93316	Human POSHL1 scann	C 637	13.2	9.5	29	14	AAZ53644	Nucleic acid ligand
C 565	13.2	9.5	25	24	ABV93317	Human POSHL1 scann	C 638	13.2	9.5	29	17	AAZ07683	NGF SELEX clone ng
C 566	13.2	9.5	25	24	ABV93318	Human POSHL1 scann	C 639	13.2	9.5	29	18	AAZ00772	SELEX ligand ngf.k
C 567	13.2	9.5	25	24	ABV93319	Human POSHL1 scann	C 640	13.2	9.5	29	19	AAZ14553	SELEX identified l
C 568	13.2	9.5	25	24	ABT03727	Human Otx-1 gene p	C 641	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 569	13.2	9.5	25	24	ABO13124	Oligonucleotide ad	C 642	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 570	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 643	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 571	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 644	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 572	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 645	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 573	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 646	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 574	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 647	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 575	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 648	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 576	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 649	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 577	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 650	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 578	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 651	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 579	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 652	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 580	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 653	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 581	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 654	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 582	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 655	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 583	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 656	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 584	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 657	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 585	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 658	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 586	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 659	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 587	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 660	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 588	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 661	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 589	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 662	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 590	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 663	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 591	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 664	13.2	9.5	29	20	AAZ58977	SELEX identified l
C 592	13.2	9.5	25	24	ABO13124	Human GDMPLP-1 25-m	C 665	13.2	9.5	29	20	AAZ58977	SELEX identified l

666	13.2	9.5	30	24	ABN81356	Thermus cytochrome	C 739	13	9.4	25	24	ABN81356	Real-time PCR prob
667	13	9.4	13	23	ABC47950	Oligonucleotide SE	C 740	13	9.4	25	24	ABK87814	Human Kail (K1) pr
668	13	9.4	13	23	ABC47951	Oligonucleotide SE	C 741	13	9.4	25	24	AEN04201	Human GDMPL-1 25-m
669	13	9.4	13	23	ABF16654	Oligonucleotide SE	C 742	13	9.4	25	24	AEN04202	Human GDMPL-1 25-m
670	13	9.4	13	23	ABF16655	Oligonucleotide SE	C 743	13	9.4	25	24	AEN04203	Human GDMPL-1 25-m
671	13	9.4	15	17	ABT50323	Rabbit CTRP HH rib	C 744	13	9.4	25	24	AEN04204	Human GDMPL-1 25-m
672	13	9.4	20	25	ACC40945	Human superoxide d	C 745	13	9.4	25	24	ABN04205	Human GDMPL-1 25-m
673	13	9.4	21	16	AAQ97540	Primer 1318 for hu	C 746	13	9.4	26	13	AAQ24937	Chicken alpha-glob
674	13	9.4	21	17	AAQ38148	Primer X for DNA p	C 747	13	9.4	26	13	AAQ24938	Chicken alpha-glob
675	13	9.4	21	21	AAQ22132	Arabidopsis thalia	C 748	13	9.4	26	13	AAQ24939	Primer to amplify
676	13	9.4	21	21	AAQ36959	Human dysferlin ex	C 749	13	9.4	26	13	AAQ24940	Chlamydia 16S ribo
677	13	9.4	21	21	AAQ252317	Rat neuronal T-typ	C 750	13	9.4	26	16	AAQ80502	Oligonucleotide us
678	13	9.4	21	21	AAH1504	Human ADH7 gene ex	C 751	13	9.4	26	19	AAV66860	Human VSGF 121-res
679	13	9.4	21	22	AAH19683	Murine MSK-2 cDNA	C 752	13	9.4	26	22	AAQ18691	Human H11 coding s
680	13	9.4	21	22	AAH19683	Stenotrophomonas s	C 753	13	9.4	26	22	AAQ18691	Human DISC1/DISC2
681	13	9.4	21	24	AAH19683	Human MUH1 cDNA am	C 754	13	9.4	26	22	AAQ18691	Human vascular end
682	13	9.4	21	24	AAH19683	Human chromosome 1	C 755	13	9.4	26	22	AAQ18691	Human gene specifi
683	13	9.4	21	24	AAH19683	Aspergillus niger	C 756	13	9.4	26	22	AAQ18691	PCR primer #2 to a
684	13	9.4	21	24	AAH19683	DNA repair protein	C 757	13	9.4	26	22	AAQ18691	Delta-9 desaturase
685	13	9.4	21	24	AAH19683	ygeJ gene specific	C 758	13	9.4	26	22	AAQ18691	PCR primer for the
686	13	9.4	21	24	AAH19683	Glyceroldehyde-3-P	C 759	13	9.4	26	22	AAQ18691	Saccharomyces cere
687	13	9.4	21	24	AAH19683	HIV-2 (LAV2C) sens	C 760	13	9.4	26	22	AAQ18691	Carcinoma embryonic a
688	13	9.4	21	24	AAH19683	Chlamydia pneumonia	C 761	13	9.4	26	22	AAQ18691	Thujia plicata Tp4
689	13	9.4	21	24	AAH19683	PCR primer used to	C 762	13	9.4	26	22	AAQ18691	Cowpea neoxanthin
690	13	9.4	21	24	AAH19683	Human myc PCR prim	C 763	13	9.4	26	22	AAQ18691	Toxicologically re
691	13	9.4	21	24	AAH19683	5'-PCR primer for	C 764	13	9.4	26	22	AAQ18691	S. peregrina cyste
692	13	9.4	21	24	AAH19683	Murine OAS gene is	C 765	13	9.4	26	22	AAQ18691	Adapter for TaqI r
693	13	9.4	21	24	AAH19683	Human RTO-PCR prim	C 766	13	9.4	26	22	AAQ18691	Foxi digested olig
694	13	9.4	21	24	AAH19683	Oat HASGT cDNA PCR	C 767	13	9.4	26	22	AAQ18691	Human p25 PCR prim
695	13	9.4	21	24	AAH19683	PCR primer for FcI	C 768	13	9.4	26	22	AAQ18691	Mutated DK-1 fragm
696	13	9.4	21	24	AAH19683	Bovine HS-glycopro	C 769	13	9.4	26	22	AAQ18691	Human complement f
697	13	9.4	21	24	AAH19683	C. albicans sterol	C 770	13	9.4	26	22	AAQ18691	Human secreted pro
698	13	9.4	21	24	AAH19683	Human liver cancer	C 771	13	9.4	26	22	AAQ18691	Primer-1 for N. ta
699	13	9.4	21	24	AAH19683	Multiplex group PC	C 772	13	9.4	26	22	AAQ18691	Polymorphic fragme
700	13	9.4	21	24	AAH19683	PCR primer INF7 f	C 773	13	9.4	26	22	AAQ18691	B subtilis pats pr
701	13	9.4	21	24	AAH19683	Reverse PCR prim	C 774	13	9.4	26	22	AAQ18691	Human BPIL 232 PCR
702	13	9.4	21	24	AAH19683	Human ATP-depend	C 775	13	9.4	26	22	AAQ18691	Human polynucleoti
703	13	9.4	21	24	AAH19683	Flanking sequence	C 776	13	9.4	26	22	AAQ18691	Human GPCR DNA cl
704	13	9.4	21	24	AAH19683	Human shear factor	C 777	13	9.4	26	22	AAQ18691	Breast cancer mark
705	13	9.4	21	24	AAH19683	Human LCAT gene fo	C 778	13	9.4	26	22	AAQ18691	N-terminus probe u
706	13	9.4	21	24	AAH19683	Human large protei	C 779	13	9.4	26	22	AAQ18691	HBV amplifier prob
707	13	9.4	21	24	AAH19683	Human growth hormo	C 780	13	9.4	26	22	AAQ18691	Thrombin DNA ligan
708	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 781	13	9.4	26	22	AAQ18691	Chromosome 11 (loc
709	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 782	13	9.4	26	22	AAQ18691	PCR primer 2 used
710	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 783	13	9.4	26	22	AAQ18691	RIN genomic DNA fr
711	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 784	13	9.4	26	22	AAQ18691	RIN genomic DNA PC
712	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 785	13	9.4	26	22	AAQ18691	PCR primer for the
713	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 786	13	9.4	26	22	AAQ18691	DR5 extracellular
714	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 787	13	9.4	26	22	AAQ18691	HBV 84 amplifier p
715	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 788	13	9.4	26	22	AAQ18691	Human alpha 1 coll
716	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 789	13	9.4	26	22	AAQ18691	PCR primer for mut
717	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 790	13	9.4	26	22	AAQ18691	Macrophage stimula
718	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 791	13	9.4	26	22	AAQ18691	Amplifier probe HB
719	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 792	13	9.4	26	22	AAQ18691	Human DR5 PCR prim
720	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 793	13	9.4	26	22	AAQ18691	PCR primer for amp
721	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 794	13	9.4	26	22	AAQ18691	Promoter region of
722	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 795	13	9.4	26	22	AAQ18691	Human detact forwar
723	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 796	13	9.4	26	22	AAQ18691	Rat hexokinase 1 g
724	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 797	13	9.4	26	22	AAQ18691	Enterococcus faeci
725	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 798	13	9.4	26	22	AAQ18691	Thrombin high affi
726	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 799	13	9.4	26	22	AAQ18691	Novel Helicobacter
727	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 800	13	9.4	26	22	AAQ18691	Novel Helicobacter
728	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 801	13	9.4	26	22	AAQ18691	Human TR430 recept
729	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 802	13	9.4	26	22	AAQ18691	
730	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 803	13	9.4	26	22	AAQ18691	
731	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 804	13	9.4	26	22	AAQ18691	
732	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 805	13	9.4	26	22	AAQ18691	
733	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 806	13	9.4	26	22	AAQ18691	
734	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 807	13	9.4	26	22	AAQ18691	
735	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 808	13	9.4	26	22	AAQ18691	
736	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 809	13	9.4	26	22	AAQ18691	
737	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 810	13	9.4	26	22	AAQ18691	
738	13	9.4	21	24	AAH19683	Oligonucleotide ad	C 811	13	9.4	26	22	AAQ18691	

812	13	9.4	30	24	ABK94875	Pat regulated gene
813	13	9.4	30	24	ABK94860	Degenerate PCR pri
814	13	9.4	30	24	ABA98688	Human SSA-56kDa PC
815	13	9.4	30	25	ABZ70455	Mouse TREM-1 forwa
816	12.8	9.2	17	16	AAQ91452	Dysprosium (III) t
817	12.8	9.2	17	18	AAZ75159	Mouse flt-1 VEGF r
818	12.8	9.2	17	19	AAV07298	Metallotexaphyrin-
819	12.8	9.2	17	20	AAV93414	Human B-raf subatr
820	12.8	9.2	17	20	AAV93413	Human B-raf subatr
821	12.8	9.2	17	20	AAV91007	Human C-raf target
822	12.8	9.2	17	21	AAZ79844	Hepatitis B virus
823	12.8	9.2	17	24	ABZ97987	Human urokinase ge
824	12.8	9.2	17	24	ABK17683	Human ERG hamerthe
825	12.8	9.2	17	24	ABK17683	Human ERG G-cleave
826	12.8	9.2	17	24	ABL31561	Human HLA genotypi
827	12.8	9.2	18	16	AAQ91453	Dysprosium (III) t
828	12.8	9.2	18	19	AAV07301	Metallotexaphyrin-
829	12.8	9.2	18	21	AAZ92609	Antisense oligonuc
830	12.8	9.2	18	21	AAZ92642	Antisense oligonuc
831	12.8	9.2	18	21	AAV01272	Chymotrypsinogen P
832	12.8	9.2	19	19	AAV34507	BRCA1 exon 21 reve
833	12.8	9.2	19	21	AAZ82742	cdk3 ribozyme bind
834	12.8	9.2	19	21	AAZ82742	Raf-1 PCR primer
835	12.8	9.2	19	22	AAZ807015	Cell-cycle depende
836	12.8	9.2	20	16	AAH57904	Dysprosium (III) t
837	12.8	9.2	20	16	AAQ08086	Metallotexaphyrin-
838	12.8	9.2	20	20	AAV07288	PCR primer used to
839	12.8	9.2	20	20	AAZ95185	Human biallelic ma
840	12.8	9.2	20	22	AAH80477	Oligonucleotide hy
841	12.8	9.2	20	22	AAH80477	Oligonucleotide hy
842	12.8	9.2	20	22	AAH80479	Oligonucleotide hy
843	12.8	9.2	20	22	AAH80480	Oligonucleotide hy
844	12.8	9.2	20	22	AAH80481	Oligonucleotide hy
845	12.8	9.2	20	22	AAZ72122	HIV-KT PCR primer
846	12.8	9.2	20	23	ABZ72122	Gene 216 SSCP dete
847	12.8	9.2	20	23	ABZ72122	TNFR1 expression m
848	12.8	9.2	20	24	ABK70680	Human hepatocellul
849	12.8	9.2	20	24	ABK70680	Human hepatocellul
850	12.8	9.2	20	24	ABK70698	TRAK detection pr
851	12.8	9.2	20	24	AAZ72572	Murine SAC1 gene-s
852	12.8	9.2	20	24	AAZ72572	Human TRAK-2 cDNA
853	12.8	9.2	20	24	AAZ72572	Human chromosome 1
854	12.8	9.2	20	24	AAZ72572	Human COPD related
855	12.8	9.2	20	25	ACC46833	Human gene 216 pol
856	12.8	9.2	20	25	ABX74975	Human gene 216 pol
857	12.8	9.2	20	25	ABX75035	Mouse ank gene PCR
858	12.8	9.2	20	25	ABZ22323	Human gene single
859	12.8	9.2	20	25	ABZ22323	Human polymorphic
860	12.8	9.2	21	23	AAH95385	Mouse B1 repetitiv
861	12.8	9.2	21	23	AAH95385	Human mutant KCMQ2
862	12.8	9.2	22	18	AAH95385	Sense PCR primer u
863	12.8	9.2	22	20	AAZ74265	Plant vector PCR p
864	12.8	9.2	22	20	AAZ74265	Mycoplasma protect
865	12.8	9.2	22	20	AAZ74265	HIV-1 long termina
866	12.8	9.2	22	20	AAZ74265	CSF clones A14, B9
867	12.8	9.2	22	20	AAZ74265	Cytochrome c oxida
868	12.8	9.2	22	20	AAZ74265	PCR primer for the
869	12.8	9.2	22	20	AAZ74265	HG694A-24 primer
870	12.8	9.2	22	20	AAZ74265	Tyrosine phosphata
871	12.8	9.2	22	20	AAZ74265	HIV-1 long termina
872	12.8	9.2	22	20	AAZ74265	Human PRO1281 hybr
873	12.8	9.2	22	20	AAZ74265	Forward primer use
874	12.8	9.2	22	20	AAZ74265	Human dysferlin PC
875	12.8	9.2	22	20	AAZ74265	Human dysferlin PC
876	12.8	9.2	22	20	AAZ74265	PCR primer RFC1600
877	12.8	9.2	22	20	AAZ74265	Human DNA polymera
878	12.8	9.2	22	20	AAZ74265	Rat pro-collagen t
879	12.8	9.2	22	20	AAZ74265	Human PRO1281 hybr
880	12.8	9.2	22	20	AAZ74265	Human COP9 subunit
881	12.8	9.2	22	20	AAZ74265	Nucleic acid detec
882	12.8	9.2	22	20	AAZ74265	
883	12.8	9.2	22	20	AAZ74265	
884	12.8	9.2	22	20	AAZ74265	
885	12.8	9.2	24	24	ABK85949	Human beta globin
886	12.8	9.2	24	24	ABK85949	Human retinoblasto
887	12.8	9.2	24	24	ABK85949	PAR-1B control oli
888	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
889	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
890	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
891	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
892	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
893	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
894	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
895	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
896	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
897	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
898	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
899	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
900	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
901	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
902	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
903	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
904	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
905	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
906	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
907	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
908	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
909	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
910	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
911	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
912	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
913	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
914	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
915	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
916	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
917	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
918	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
919	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
920	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
921	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
922	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
923	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
924	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
925	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
926	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
927	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
928	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
929	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
930	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
931	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
932	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
933	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
934	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
935	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
936	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
937	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
938	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
939	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
940	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
941	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
942	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
943	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
944	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
945	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
946	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
947	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
948	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
949	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
950	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
951	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
952	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
953	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
954	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
955	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
956	12.8	9.2	24	24	ABK85949	Oligonucleotide ad
957	12.8	9.2	24	24	ABK85949	Oligonucleotide ad

Probe MTB030 for M
Mycobacterium tube
Sequence of juncti
HIV-1 mRNA region
Grand fir monoterp
Human gene specifi
Human obesity poly
Oligonucleotide an
Cyt di primer (CDI
Wild type HIV-1 TA
HIV-1 TAR bulge su
Oligonucleotide ta
Oligonucleotide 10
c-mpl receptor ago
Primer 109-5' for
Oligonucleotide SE
T. aestivum Dga44
HIV-1 oligonucleot
3' PCR primer used
Human inflammatory
SNP specific SNPE
PCR primer GSP1 fo
PCR primer, #2, us
Human V gene libra
HLA-A capture olig
Human NADH dehydro
PCR primer for amp
Human anti-TIMP-1
Sequence of probe
Fragment of human
Reverse-Frame HGV
Primer GE-9R for H
Pig myogenin gene
PCR primer GE-9R u
HGV primer GE-9R D
Primer used to scr
PCR primer used to
US856134 Seq ID 4
Hepatitis G virus
Reverse PCR primer

ALIGNMENTS

RESULT 1
AAI66686/c
ID AAI66686 standard; DNA; 21 BP.
AC AAI66686;
07-JAN-2002 (first entry)
Human CETP DNA related PCR primer.
CETP; arteriosclerosis; cholesterol ester transfer protein; HDL;
high density lipoprotein; human; PCR primer; ss.
Homo sapiens.
WO200171032-A1.
27-SEP-2001.
23-MAR-2001; 2001WO-JP02327.
24-MAR-2000; 2000JP-0084264.
(BMLB-) BML INC.
XX

PI Nagano M, Ito M, Sagehashi Y, Hattori H, Egashira T, Yamashita S;
PI Matsuzawa Y;
DR WPI; 2001-611516/70.
XX
XX Determining a risk factor for arteriosclerosis comprises detecting
PT mutations in genes for cholesterol ester transfer protein.
XX
XX Disclosure; Page 21; 59pp; Japanese.
XX
XX The invention relates to detecting the risk factor for arteriosclerosis
CC in a subject that involves detecting mutations in the gene for
CC cholesterol ester transfer protein (CETP) related to the degree of risk
CC of arteriosclerosis. The mutant proteins alter the level of HDL in the
CC blood. The high frequency mutations can be detected for prevention and
CC treatment of arteriosclerosis. Sequences AAI6655-91 represent PCR
CC primers related to the human CETP DNA, used during the course of the
CC invention.
XX
XX Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 other;

Query Match 15.1%; Score 21; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 TCACAGCTGACCCCTGGTGT 55
Db 21 TCACAGCTGACCCCTGGTGT 1

RESULT 2
ABT13031/c
ID ABT13031 standard; DNA; 20 BP.
XX
XX AC ABT13031;
XX
XX DT 30-JAN-2003 (first entry)
XX
XX DE Human cholesterol ester transfer protein PCR primer (SNP specific) #12.
XX
XX KW Human; PCR; primer; ss; gene therapy; single nucleotide polymorphism;
KW cytochrome C oxidase subunit VIB; COX6B; high serum cholesterol; GRI-1;
KW N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;
KW glycosylphosphatidylinositol-1; SNP; low serum high density lipoprotein.
XX
XX OS Homo sapiens.
XX
XX PN WO200272604-A2.
XX
XX PD 19-SEP-2002.
XX
XX PF 05-MAR-2002; 2002WO-US06728.
XX
XX PR 09-MAR-2001; 2001US-0802640.
XX
XX PA (SEQU-) SEQUENOM INC.
XX
XX PI Braun A, Bansal A, Kleya PW;
XX
XX DR WPI; 2002-750478/81.
XX
XX

PT Detecting the presence or absence of an allelic variant of a
PT polymorphic region of COX6B and/or GRI-1 gene, useful for detecting a
PT predisposition to high serum cholesterol, low serum HDL and
PT cardiovascular disease
XX
XX Disclosure; Page 30; 199pp; English.

XX The invention comprises methods of detecting the presence or absence of
CC at least one allelic variant of a polymorphic region of a gene associated
CC with cardiovascular disease. The invention specifically relates to
CC detecting the region of a cytochrome C oxidase subunit VIB (COX6B) gene
CC that is associated with high serum cholesterol, or the region of the

CC N-acetylglucosaminyl transferase component glycosylphosphatidylinositol-1
 CC (GPI-1) gene that is associated with low serum high density lipoprotein
 CC (HDL). The methods of the invention are useful for detecting a
 CC predisposition to high serum cholesterol, low serum HDL and
 CC cardiovascular disease. The methods are also useful for elucidating
 CC pathological pathways, developing diagnostic assays and new drug
 CC therapies for such disorders. The present DNA sequence represents a PCR
 CC primer used to amplify a human gene that is associated with high serum
 CC cholesterol, low serum HDL and/or cardiovascular disease.
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 other;

Query Match 14.4%; Score 20; DB 24; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTTGTAGCAGAGGCGAACA 28
 |||||
 DB 20 CTTGTAGCAGAGGCGAACA 1

RESULT 3

ABX12175/c

ID ABX12175 standard; DNA; 20 BP.

XX
 AC ABX12175;

DT 16-MAY-2003 (first entry)

XX Human cholesteryl ester transfer protein, reverse PCR primer.

XX Human; cholesteryl ester transfer protein; lipid metabolism;

XX cholesterol metabolism; atherosclerosis; cardiovascular disease;

XX antisense; PCR; primer; ss.

XX Homo sapiens.

XX WO2003014306-A2.

XX 20-FEB-2003.

XX 05-AUG-2002; 2002WO-US24919.

XX 08-AUG-2001; 2001US-0925139.

XX (ISIS-) ISIS PHARM INC.

XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;

XX WPI; 2003-248014/25.

XX New antisense compound, useful for preparing a composition for treating

XX abnormal lipid or cholesterol metabolism, atherosclerosis or

XX cardiovascular disease

XX Example 13; Page 93; 114pp; English.

XX The invention relates to new antisense compounds targeted to a nucleic

XX acid molecule encoding human cholesteryl ester transfer protein,

XX specifically hybridizes with it and inhibits the expression of human

XX cholesteryl ester transfer protein. The compound is useful for preparing

XX a composition for treating abnormal lipid or cholesterol metabolism,

XX atherosclerosis or cardiovascular disease. The present sequence

XX represents a human cholesteryl ester transfer protein, PCR primer.

XX Sequence 20 BP; 6 A; 10 C; 1 G; 3 T; 0 other;

Query Match 14.4%; Score 20; DB 25; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.3e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 CGTGTGGAAGTGGGTAG 84
 |||||

DB 20 CGTGTGGAAGTGGGTAG 1

RESULT 4

ABX12198/c

ID ABX12198 standard; DNA; 20 BP.

XX
 AC ABX12198;

DT 16-MAY-2003 (first entry)

XX Human cholesteryl ester transfer protein, antisense oligo #19.

XX Human; cholesteryl ester transfer protein; lipid metabolism;

XX cholesterol metabolism; atherosclerosis; cardiovascular disease;

XX antisense; probe; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX modified_base 1..6

XX /mod_base= OTHER

XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX modified_base 1..20

XX /mod_base= OTHER

XX /note= "Phosphorothioate nucleotides; all cytidine

XX residues are 5-methylcytidines"

XX modified_base 15..20

XX /mod_base= OTHER

XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003014306-A2.

XX 20-FEB-2003.

XX 05-AUG-2002; 2002WO-US24919.

XX 08-AUG-2001; 2001US-0925139.

XX (ISIS-) ISIS PHARM INC.

XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;

XX WPI; 2003-248014/25.

XX New antisense compound, useful for preparing a composition for treating

XX abnormal lipid or cholesterol metabolism, atherosclerosis or

XX cardiovascular disease

XX Claim 3; Page 96; 114pp; English.

XX The invention relates to new antisense compounds targeted to a nucleic

XX acid molecule encoding human cholesteryl ester transfer protein,

XX specifically hybridizes with it and inhibits the expression of human

XX cholesteryl ester transfer protein. The compound is useful for preparing

XX a composition for treating abnormal lipid or cholesterol metabolism,

XX atherosclerosis or cardiovascular disease. The present sequence

XX represents a human cholesteryl ester transfer protein, antisense

XX oligonucleotide of the invention.

XX Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 other;

Query Match 14.4%; Score 20; DB 25; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.3e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATGGGCTGTAGCAGAA 20
 |||||

DB 20 GGATGGGCTGTAGCAGAA 1

RESULT 5

ABX12199/c

ID ABX12199 standard; DNA; 20 BP.
XX AC ABX12199;
XX DT 16-MAY-2003 (first entry)
XX DE Human cholesteryl ester transfer protein, antisense oligo #20.
XX KW Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
XX antisense; probe; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT modified_base 1..6
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 1..20
FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides; all cytidine
FT residues are 5-methylcytidines"
FT modified_base 15..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX PN WO2003014306-A2.
XX PD 20-FEB-2003.
XX PP 05-AUG-2002; 2002WO-US24919.
XX PR 08-AUG-2001; 2001US-0925139.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Crooke RM, Graham MJ, Nero PS, Wanciewicz E;
XX WPI; 2003-248014/25.
XX DR New antisense compound, useful for preparing a composition for treating
PT abnormal lipid or cholesterol metabolism, atherosclerosis or
PT cardiovascular disease
XX PS Claim 3; Page 96; 114pp; English.
XX CC The invention relates to new antisense compounds targeted to a nucleic
CC acid molecule encoding human cholesteryl ester transfer protein,
CC specifically hybridizes with it and inhibits the expression of human
CC cholesteryl ester transfer protein. The compound is useful for preparing
CC a composition for treating abnormal lipid or cholesterol metabolism,
CC atherosclerosis or cardiovascular disease. The present sequence
CC represents a human cholesteryl ester transfer protein, antisense
CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 6 A; 5 C; 7 G; 2 T; 0 other;
Query Match 14.4%; Score 20; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 CTGGAACCTGGTGTCCT 60
Db 20 CTGGAACCTGGTGTCCT 1
RESULT 6
ID ABX12200/c
XX AC ABX12200 standard; DNA; 20 BP.
XX AC ABX12200;
XX DT 16-MAY-2003 (first entry)

XX DE Human cholesteryl ester transfer protein, antisense oligo #21.
XX KW Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
XX antisense; probe; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT modified_base 1..6
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 1..20
FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides; all cytidine
FT residues are 5-methylcytidines"
FT modified_base 15..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX PN WO2003014306-A2.
XX PD 20-FEB-2003.
XX PP 05-AUG-2002; 2002WO-US24919.
XX PR 08-AUG-2001; 2001US-0925139.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Crooke RM, Graham MJ, Nero PS, Wanciewicz E;
XX WPI; 2003-248014/25.
XX DR New antisense compound, useful for preparing a composition for treating
PT abnormal lipid or cholesterol metabolism, atherosclerosis or
PT cardiovascular disease
XX PS Claim 3; Page 96; 114pp; English.
XX CC The invention relates to new antisense compounds targeted to a nucleic
CC acid molecule encoding human cholesteryl ester transfer protein,
CC specifically hybridizes with it and inhibits the expression of human
CC cholesteryl ester transfer protein. The compound is useful for preparing
CC a composition for treating abnormal lipid or cholesterol metabolism,
CC atherosclerosis or cardiovascular disease. The present sequence
CC represents a human cholesteryl ester transfer protein, antisense
CC oligonucleotide of the invention.
XX SQ Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 other;
Query Match 14.4%; Score 20; DB 25; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 71 GGAAGTTGGTTAGGAGTAC 90
Db 20 GGAAGTTGGTTAGGAGTAC 1
RESULT 7
ID ABX12217/c
XX AC ABX12217;
XX DT 16-MAY-2003 (first entry)
XX DE Human cholesteryl ester transfer protein, antisense oligo #38.
XX KW Human; cholesteryl ester transfer protein; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; cardiovascular disease;

antisense; probe; ss.
 KW XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 modified_base 1..6
 FT FT /mod_base= OTHER
 FT FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT FT 1..20
 FT FT /mod_base= OTHER
 FT FT /note= "Phosphorothioate nucleotides; all cytidine
 FT FT residues are 5-methylcytidines"
 FT FT 15..20
 FT FT /mod_base= OTHER
 FT FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT FT 15..20
 FT FT /mod_base= OTHER
 FT FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 PN PN WO2003014306-A2.
 XX
 XX 20-FEB-2003.
 XX
 XX 05-AUG-2002; 2002WO-US24919.
 PF PF
 XX 08-AUG-2001; 2001US-0925139.
 PR PR
 XX (ISIS-) ISIS PHARM INC.
 PA PA
 XX Crooke RM, Graham MJ, Nero PS, Wanciewicz E;
 PI PI
 XX WPI; 2003-248014/25.
 DR DR
 XX New antisense compound, useful for preparing a composition for treating
 PT abnormal lipid or cholesterol metabolism, atherosclerosis or
 PT cardiovascular disease
 PT
 XX Claim 3; Page 97; 114pp; English.
 PS
 XX The invention relates to new antisense compounds targeted to a nucleic
 CC acid molecule encoding human cholesteryl ester transfer protein,
 CC specifically hybridizes with it and inhibits the expression of human
 CC cholesteryl ester transfer protein. The compound is useful for preparing
 CC a composition for treating abnormal lipid or cholesterol metabolism,
 CC atherosclerosis or cardiovascular disease. The present sequence
 CC represents a human cholesteryl ester transfer protein, antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 other;
 Query Match 14.4%; Score 20; DB 25; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 GCTTGTAGCAGAGGCAAGC 27
 DB 20 GCTTGTAGCAGAGGCAAGC 1
 RESULT 8
 ABX12218/c
 ID ABX12218 standard; DNA; 20 BP.
 XX
 AC ABX12218;
 XX
 DT 16-MAY-2003 (first entry)
 DE Human cholesteryl ester transfer protein, antisense oligo #39.
 XX
 KW Human; cholesteryl ester transfer protein; lipid metabolism;
 KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
 KW antisense; probe; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 modified_base 1..6
 FT FT /mod_base= OTHER
 FT FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT FT 1..20
 FT FT /mod_base= OTHER
 FT FT /note= "Phosphorothioate nucleotides; all cytidine
 FT FT residues are 5-methylcytidines"
 FT FT 15..20
 FT FT /mod_base= OTHER
 FT FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 PN PN WO2003014306-A2.
 XX
 XX 20-FEB-2003.
 XX
 XX 05-AUG-2002; 2002WO-US24919.
 PF PF
 XX 08-AUG-2001; 2001US-0925139.
 PR PR
 XX (ISIS-) ISIS PHARM INC.
 PA PA
 XX Crooke RM, Graham MJ, Nero PS, Wanciewicz E;
 PI PI
 XX WPI; 2003-248014/25.
 DR DR
 XX New antisense compound, useful for preparing a composition for treating
 PT abnormal lipid or cholesterol metabolism, atherosclerosis or
 PT cardiovascular disease
 PT
 XX Claim 3; Page 97; 114pp; English.
 PS
 XX The invention relates to new antisense compounds targeted to a nucleic
 CC acid molecule encoding human cholesteryl ester transfer protein,
 CC specifically hybridizes with it and inhibits the expression of human
 CC cholesteryl ester transfer protein. The compound is useful for preparing
 CC a composition for treating abnormal lipid or cholesterol metabolism,
 CC atherosclerosis or cardiovascular disease. The present sequence
 CC represents a human cholesteryl ester transfer protein, antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 other;
 Query Match 14.4%; Score 20; DB 25; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 GCTTGTAGCAGAGGCAAGC 27
 DB 20 GCTTGTAGCAGAGGCAAGC 1
 RESULT 8
 ABX12218/c
 ID ABX12218 standard; DNA; 20 BP.
 XX
 AC ABX12218;
 XX
 DT 16-MAY-2003 (first entry)
 DE Human cholesteryl ester transfer protein, antisense oligo #39.
 XX
 KW Human; cholesteryl ester transfer protein; lipid metabolism;
 KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
 KW antisense; probe; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 modified_base 1..6
 FT FT /mod_base= OTHER
 FT FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT FT 1..20
 FT FT /mod_base= OTHER
 FT FT /note= "Phosphorothioate nucleotides; all cytidine
 FT FT residues are 5-methylcytidines"
 FT FT 15..20
 FT FT /mod_base= OTHER
 FT FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 PN PN WO2003014306-A2.
 XX
 XX 20-FEB-2003.
 XX
 XX 05-AUG-2002; 2002WO-US24919.
 PF PF
 XX 08-AUG-2001; 2001US-0925139.
 PR PR
 XX (ISIS-) ISIS PHARM INC.
 PA PA
 XX Crooke RM, Graham MJ, Nero PS, Wanciewicz E;
 PI PI
 XX WPI; 2003-248014/25.
 DR DR
 XX New antisense compound, useful for preparing a composition for treating
 PT abnormal lipid or cholesterol metabolism, atherosclerosis or
 PT cardiovascular disease
 PT
 XX Claim 3; Page 97; 114pp; English.
 PS
 XX The invention relates to new antisense compounds targeted to a nucleic
 CC acid molecule encoding human cholesteryl ester transfer protein,
 CC specifically hybridizes with it and inhibits the expression of human
 CC cholesteryl ester transfer protein. The compound is useful for preparing
 CC a composition for treating abnormal lipid or cholesterol metabolism,
 CC atherosclerosis or cardiovascular disease. The present sequence
 CC represents a human cholesteryl ester transfer protein, antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 other;
 Query Match 14.4%; Score 20; DB 25; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 GCTTGTAGCAGAGGCAAGC 27
 DB 20 GCTTGTAGCAGAGGCAAGC 1
 RESULT 9
 ABX12219/c
 ID ABX12219 standard; DNA; 20 BP.
 XX
 AC ABX12219;
 XX
 DT 16-MAY-2003 (first entry)
 DE Human cholesteryl ester transfer protein, antisense oligo #40.
 XX
 KW Human; cholesteryl ester transfer protein; lipid metabolism;
 KW cholesterol metabolism; atherosclerosis; cardiovascular disease;
 KW antisense; probe; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 modified_base 1..6
 FT FT /mod_base= OTHER
 FT FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT FT 1..20
 FT FT /mod_base= OTHER
 FT FT /note= "Phosphorothioate nucleotides; all cytidine
 FT FT residues are 5-methylcytidines"
 FT FT 15..20
 FT FT /mod_base= OTHER
 FT FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 PN PN WO2003014306-A2.
 XX
 XX 20-FEB-2003.
 XX
 XX 05-AUG-2002; 2002WO-US24919.
 PF PF
 XX 08-AUG-2001; 2001US-0925139.
 PR PR
 XX (ISIS-) ISIS PHARM INC.
 PA PA
 XX Crooke RM, Graham MJ, Nero PS, Wanciewicz E;
 PI PI
 XX WPI; 2003-248014/25.
 DR DR
 XX New antisense compound, useful for preparing a composition for treating
 PT abnormal lipid or cholesterol metabolism, atherosclerosis or
 PT cardiovascular disease
 PT
 XX Claim 3; Page 97; 114pp; English.
 PS
 XX The invention relates to new antisense compounds targeted to a nucleic
 CC acid molecule encoding human cholesteryl ester transfer protein,
 CC specifically hybridizes with it and inhibits the expression of human
 CC cholesteryl ester transfer protein. The compound is useful for preparing
 CC a composition for treating abnormal lipid or cholesterol metabolism,
 CC atherosclerosis or cardiovascular disease. The present sequence
 CC represents a human cholesteryl ester transfer protein, antisense
 CC oligonucleotide of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 10 C; 1 G; 3 T; 0 other;
 Query Match 14.4%; Score 20; DB 25; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 63 AGCGTGGTGGGAAGTTGGGTT 82
 DB 20 AGCGTGGTGGGAAGTTGGGTT 1

```
FT /note= "Phosphorothioate nucleotides; all cytidine
FT modified_base 15..20
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003014306-A2.
XX
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US24919.
XX
XX 08-AUG-2001; 2001US-0925139.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;
XX WPI; 2003-248014/25.
XX
XX New antisense compound, useful for preparing a composition for treating
XX abnormal lipid or cholesterol metabolism, atherosclerosis or
XX cardiovascular disease
XX
XX Claim 3; Page 97; 114pp; English.
XX
XX The invention relates to new antisense compounds targeted to a nucleic
XX acid molecule encoding human cholesteryl ester transfer protein,
XX specifically hybridises with it and inhibits the expression of human
XX cholesteryl ester transfer protein. The compound is useful for preparing
XX a composition for treating abnormal lipid or cholesterol metabolism,
XX atherosclerosis or cardiovascular disease. The present sequence
XX represents a human cholesteryl ester transfer protein, antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 other;
XX
XX Query Match 14.4%; Score 20; DB 25; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 4.3e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 84 GGAGTACCGAGATGGAGATT 103
XX |||||||||||||||||||
XX 20 GGAGTACCGAGATGGAGATT 1
XX
XX RESULT 10
XX ABX12220/c
XX ID ABX12220 standard; DNA; 20 BP.
XX
XX AC ABX12220;
XX
XX 16-MAY-2003 (first entry)
XX
XX Human cholesteryl ester transfer protein, antisense oligo #1.
XX
XX Human; cholesteryl ester transfer protein; lipid metabolism;
XX cholesterol metabolism; atherosclerosis; cardiovascular disease;
XX antisense; probe; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..6
XX /mod_base= OTHER
XX
XX modified_base 1..20
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX modified_base 15..20
XX /note= "Phosphorothioate nucleotides; all cytidine
XX residues are 5-methylcytidines"
XX
XX modified_base 15..20
XX /mod_base= OTHER
XX
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
```

```
XX WO2003014306-A2.
XX
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US24919.
XX
XX 08-AUG-2001; 2001US-0925139.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke RM, Graham MJ, Nero PS, Wancewicz E;
XX WPI; 2003-248014/25.
XX
XX New antisense compound, useful for preparing a composition for treating
XX abnormal lipid or cholesterol metabolism, atherosclerosis or
XX cardiovascular disease
XX
XX Claim 3; Page 97; 114pp; English.
XX
XX The invention relates to new antisense compounds targeted to a nucleic
XX acid molecule encoding human cholesteryl ester transfer protein,
XX specifically hybridises with it and inhibits the expression of human
XX cholesteryl ester transfer protein. The compound is useful for preparing
XX a composition for treating abnormal lipid or cholesterol metabolism,
XX atherosclerosis or cardiovascular disease. The present sequence
XX represents a human cholesteryl ester transfer protein, antisense
XX oligonucleotide of the invention.
XX
XX Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 other;
XX
XX Query Match 14.4%; Score 20; DB 25; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 4.3e+03;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 120 CTATCTTAAGGCCCACTGG 139
XX |||||||||||||||||||
XX 20 CTATCTTAAGGCCCACTGG 1
XX
XX RESULT 11
XX AAT50642
XX ID AAT50642 standard; RNA; 18 BP.
XX
XX AC AAT50642;
XX
XX 10-MAR-1997 (first entry)
XX
XX Human CETP hairpin ribozyme target sequence #1669.
XX
XX Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
XX neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
XX reverse cholesterol transport; high density lipoprotein; therapy; CETP;
XX familial hypercholesterolaemia; dyslipidaemia; hypolipoproteinaemia;
XX peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
XX angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
XX LDL; ss.
XX
XX Homo sapiens.
XX
XX WO9620279-A1.
XX
XX 04-JUL-1996.
XX
XX 11-DEC-1995; 95WO-US16000.
XX
XX 23-DEC-1994; 94US-0363240.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX (WARN ) WARNER LAMBERT CO.
XX
XX Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
```

XX DR WPI; 1996-321852/32.

XX PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA

XX PT - useful for preventing or treating initial development, progression

XX PT or regression of vascular diseases, esp. familial

XX PT hypercholesterolaemia

XX PS Claim 4; Page 54; 72pp; English.

XX CC AAT50595-T50642 represent target sequences for the human cholesterol

XX CC ester transfer protein (CETP) hairpin ribozymes (see AAT50547-T50594).

XX CC CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer

XX CC between plasma lipoproteins. The numbering of the targets refers to the

XX CC position of the cleavage site in full length CETP. The ribozyme then

XX CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The

XX CC ribozymes are able to cleave mRNA from the gene encoding CETP, thereby

XX CC blocking synthesis and/or expression of the mRNA. By inhibiting CETP,

XX CC the reverse cholesterol transport (RCT) pathway can be inhibited (or

XX CC eliminated) thereby preventing the reduction in size density of the high

XX CC density lipoproteins (HDL), prolonging HDL half life, and therefore

XX CC increasing HDL levels. The ribozymes can be used to treat conditions

XX CC associated with abnormal levels of CETP, specifically atherosclerosis,

XX CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,

XX CC familial hypercholesterolaemia, hypobetalipoproteinaemia, vascular

XX CC complications of diabetes, transplant, atherectomy and angioplastic

XX CC restenosis. By inhibiting CETP, the levels of HDL and low density

XX CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a

XX CC decrease in LDL levels, and a corresponding increase in HDL levels). The

XX CC ribozymes can also be used diagnostically to study genetic drift and

XX CC mutations in diseased cells, and to detect CETP mRNA. As the ribozymes

XX CC target specific regions of the CETP gene, they have low non-specific

XX CC activity.

XX SQ Sequence 18 BP; 4 A; 7 C; 4 G; 3 U; 0 other;

Query Match 12.98; Score 18; DB 17; Length 18;

Best Local Similarity 83.3%; Pred. No. 1.9e+04;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 33 GCTCACAGCTGGACCT 50

DB 1 GCUCACAGCUGGACCCU 18

RESULT 12

AAX37644

ID AAX37644 standard; DNA; 22 BP.

AC AAX37644;

XX 08-JUL-1999 (first entry)

XX DT HBV detecting primer 8.

XX DE

XX KB Detection; HBV; real time; PCR; reporter; fluorescent; primer;

XX KW quencher; fluorescence resonance energy transfer; ss.

XX OS Synthetic.

XX OS Hepatitis B virus.

XX PN JP11103897-A.

XX PD 20-APR-1999.

XX PF 30-SEP-1997; 97JP-0282612.

XX PR 30-SEP-1997; 97JP-0282612.

XX (SRLS-) SRL KK.

XX PA WPI; 1999-305860/26.

XX DR

XX CC

PT New primers and probes - for measurement of an Herpes B Virus (HBV)

PT gene by a real time detecting PCR

XX PS Example 2; Page 8; 12pp; Japanese.

XX CC This invention describes a method for the measurement of an HBV gene by

XX CC a real time detecting PCR. The invention also describes a method for the

XX CC measurement of an HBV gene by a real time detecting PCR in which a

XX CC reporter fluorescent colour and a quencher fluorescent colour are

XX CC combined to an oligonucleotide, the fluorescence of said reporter

XX CC fluorescent colour is controlled by fluorescence resonance energy

XX CC transfer when reporter fluorescent colour is combined to the same probe

XX CC as quencher fluorescent colour. The method can measure an HBV exactly in

XX CC a high sensitivity.

XX SQ Sequence 22 BP; 5 A; 11 C; 1 G; 5 T; 0 other;

Query Match 12.4%; Score 17.2; DB 20; Length 22;

Best Local Similarity 86.4%; Pred. No. 3.6e+04;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 108 CCCAAGCTCTCCCTATCTCTAAA 129

DB 1 CCCAAGCTCTCCCTATCTCTAAA 22

RESULT 13

AAX22550/C

ID AAX22550 standard; mRNA; 17 BP.

XX AC AAX22550;

XX DT 21-MAY-1999 (first entry)

XX DE Human CETP RNA fragment #5.

XX KW CETP; cholesterol ester transfer protein; inhibitor; therapy; treatment;

XX KW surface plasmon resonance; vascular disease; pathogenic; atherosclerosis;

XX KW human; ss.

XX OS Homo sapiens.

XX PN DE19731609-A1.

XX PD 18-FEB-1999.

XX PF 23-JUL-1997; 97DE-1031609.

XX PR 23-JUL-1997; 97DE-1031609.

XX (BOEH) BOEHRINGER INGELHEIM PHARMA KG.

XX PI Budzinski R, Krist B, Mark M, Mueller P;

XX DR WPI; 1999-143775/13.

XX PT RNA transcript of human cholesteryl ester transfer protein gene -

XX PT useful in drug screening assays, especially for atherosclerosis

XX PS Disclosure; Page 13; 24pp; German.

XX CC This invention describes the isolation of a transcript of the human

XX CC cholesteryl ester transfer protein (CETP) gene having a 5' untranslated

XX CC region including a regulatory sequence. The invention also describes

XX CC a method (a) for identifying substances capable of inhibiting CETP gene

XX CC expression, comprising measuring the translation rate of the above

XX CC transcript in the presence of a test substance, (2) a test substance

XX CC capable of inhibiting CETP gene expression, (3) an antisense

XX CC oligonucleotide capable of binding to the 5' untranslated region of the

XX CC above transcript and (4) a method based on surface plasmon resonance for

XX CC measuring the binding of a substance to a nucleic acid. The test

XX CC substance of (2) and the oligonucleotide of (3) are useful for

XX CC prophylactic or therapeutic treatment of vascular diseases in which CETP

CC has a pathogenic role, especially atherosclerosis.

XX Sequence 17 BP; 2 A; 8 C; 1 G; 6 U; 0 other;

SQ Query Match 12.2%; Score 17; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GAGTACGGAGATGGAGA 101
| | | | | | | | | | | | | | | | | | | | | |
Db 17 GAGTACGGAGATGGAGA 1

RESULT 14
AAI99829
ID AAI99829 standard; DNA; 21 BP.

XX AC AAI99829;
XX DT 28-JAN-2002 (first entry)
XX DE Human G protein-coupled receptor protein TGR5 PCR primer SEQ ID NO 5.
XX KW Human; TGR5; G protein-coupled receptor protein; cerebroprotective;
XX KW cardiac; immunomodulator; cytotatic; antiinflammatory; antidiabetic;
XX KW cancer; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO20017325-A1.
XX PD 18-OCT-2001.
XX PF 12-APR-2001; 2001WO-JP03143.
XX PR 12-APR-2000; 2000JP-0110765.
XX PA (TAKE) TAKEDA CHEM IND LTD.
XX PI Miwa M, Matsui H, Shintani Y;
XX WPI; 2002-010910/01.
XX Human brain-originated G protein-coupled receptor protein TGR5,
PT applicable in diagnosis and developing drugs for diseases of e.g.
PT central nervous system and digestive organs, inflammation, cancer and
PT diabetes -
XX Example 2; Page 98; 104pp; Japanese.

XX The invention relates to a novel human G protein-coupled receptor protein
CC TGR5 and the encoding cDNA with cerebroprotective, cardiac,
CC immunomodulator, cytotatic, antiinflammatory and antidiabetic activity.
CC The protein, encoded DNA and anti-TGR5 antibody are applicable in
CC diagnosis and developing drugs for diseases of central nervous system and
CC circulatory organs, inflammation, cancer and diabetes. The present
CC sequence is that of a TGR5 PCR primer of the invention.

XX Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;

SQ Query Match 12.1%; Score 16.8; DB 24; Length 21;
Best Local Similarity 90.0%; Pred. No. 4.8e+04;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 102 TTGGCTCCCAACTCTCCCT 121
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TTGGCTCCCAACTCTCTCTT 20

RESULT 15
AAI21403
ID AAI21403 standard; DNA; 27 BP.

XX

AC AAX21403;
XX DT 21-MAY-1999 (first entry)
XX DE T.ni acyl-CoA delta-11-desaturase primer 5'-delta-9d1.
XX KW Membrane; acyl-CoA delta-11 desaturase; pheromone gland; moth; primer;
XX KW fatty acyl-CoA reactant; attraction; insect; trap; PCR; ss.
XX OS Synthetic.
XX OS Trichoplusia ni.
XX PN US5876994-A.
XX PD 02-MAR-1999.
XX PF 16-NOV-1995; 95US-0558823.
XX PR 16-NOV-1995; 95US-0558823.
XX PA (CORR) CORNELL RES FOUND INC.
XX PI Knipple DC, Miller SJ, Roelofs WL;
XX WPI; 1999-189641/16.
XX New isolated acyl-CoA desaturase - obtained from the pheromone
PT glands of insects, used for the production of unsaturated fatty
PT acyl-CoA products which can be used for pheromone production
XX Example 4; Column 22; 37pp; English.

XX Primers AAX21402-X21403 were used to PCR amplify a fragment of the
CC coding region of the membrane-associated acyl-CoA delta-11 desaturase
CC (AAX21401) expressed in the pheromone gland of the moth Trichoplusia ni.
CC The coding sequence (AAX21400) encodes a protein which contains the
CC generic motifs: His-Xaa(4)-His, His-Xaa(2)-His-His or
CC His-Xaa(4)-His-Xaa(30)-His-Xaa(2)-His-His-Xaa(135)-His-Xaa(2)-His-His.
CC The desaturase can be used to produce a pheromone precursor by converting
CC a saturated or unsaturated fatty acyl-CoA reactant to an unsaturated
CC fatty acyl-CoA product which contains at least one more carbon-carbon
CC double bond than the fatty acyl-CoA reactant. The mono-, di-, or
CC poly-unsaturated fatty acid products obtained are useful as intermediates
CC for the synthesis of diverse compounds that can be used as pheromones to
CC attract particular species of insects, especially to a trap, where they
CC can be restrained or killed.

XX Sequence 27 BP; 4 A; 4 C; 4 G; 7 T; 8 other;

SQ Query Match 12.1%; Score 16.8; DB 20; Length 27;
Best Local Similarity 57.7%; Pred. No. 5.1e+04;
Matches 15; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 58 CCTCCAGCGTGTGGAAGTTGGGTTA 83
| | | | | | | | | | | | | | | | | | | | | |
Db 2 CCTTCAGTGTGTGWTATGTGWA 27

RESULT 16
AAI14772
ID AAI14772 standard; cDNA; 30 BP.

XX AC AAI14772;
XX DT 29-JAN-2002 (first entry)
XX DE Chicken II gonadotropin-releasing hormone (GnRH) analogue cDNA.
XX KW GnRH; gonadotropin-releasing hormone; extra-pituitary GnRH receptor; ss;
XX KW antitumour; cytostatic; mammal; post-proline peptidase; endopeptidase;
XX KW blood; cell proliferation; metastasis; apoptosis; tumour regression;
XX KW proliferative disorder; chicken; chicken II GnRH analogue; cancer;
XX KW protein degradation.

OS OS Gallus gallus.

XX Key Location/Qualifiers

XX CDS 1..30

XX /*tag= a

XX /product= "Chicken II GnRH analogue peptide"

XX /transl_except= (pos:1..3, aa:Glu)

XX /transl_except= (pos:16..18, aa:Arg)

XX /partial

XX /note= "No start or stop codon"

XX WO200174377-A1.

XX 11-OCT-2001.

XX 26-SEP-2000; 2000WO-US26575.

XX 31-MAR-2000; 2000US-0540685.

XX (KHOD/) SILER-KHODR T M.

XX (KHOD/) KHODR G S.

XX Siler-Khodr TM, Khodr GS;

XX WPI; 2001-662948/76.

XX P-PSDB; AAU08771.

XX Non-mammalian gonadotropin-releasing hormone analogue capable of binding to hormone receptors in tumour cell with greater affinity and resistant to degradation by tumour tissue enzymes, useful in tumour growth regulation

XX Claim 12; Page 39; 49pp; English.

XX The invention relates to a composition comprising a non-mammalian gonadotropin-releasing hormone (GnRH) analogue for regulating tumour GnRH activity, where the analogue is capable of binding to extra-pituitary GnRH receptors expressed on tumour tissues. The analogue has a greater binding affinity than mammalian GnRH and is resistant to degradation by post-proline peptidases, particularly those found around tumour tissues, and endopeptidases found circulating in the blood. GnRH analogues are useful for regulating tumour activity by acting as superagonists at tumour tissue, leading to tissue receptor down regulation. The peptides act to reduce tumour cell proliferation and metastasis and can induce apoptosis and tumour regression. GnRH analogues are also useful for producing antibodies that specifically bind to non-mammalian GnRH peptide sequences or to tumour tissues or any other non-pituitary GnRH peptide or protein, for the treatment of proliferative disorders. This sequence represents cDNA encoding a chicken II GnRH analogue peptide.

XX Sequence 30 BP; 5 A; 8 C; 9 G; 8 T; 0 other;

XX Query Match 12.1%; Score 16.8; DB 22; Length 30;

XX Best Local Similarity 75.0%; Pred. No. 5.3e+04;

XX Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

XX 25 AGCACCAGGCTCACAGCTGGAACCCCTGG 52

XX ||||| ||||| ||||| ||||| |||||

XX 2 AGCACTGGTCTCATGGCTGATACCTGG 29

XX RESULT 17

XX AAD44973

XX ID AAD44973 standard; cDNA; 30 BP.

XX AC AAD44973;

XX 27-DEC-2002 (first entry)

XX Chicken gonadotropin releasing hormone (GnRH) cDNA.

XX Chicken; gonadotropin releasing hormone; postcoital contraceptive agent;

XX GnRH; pregnancy; ovarian cyst; endometriosis; polycystic ovarian disease; leiomyomas; luteolytic agent; fertility regulation; menses-inducing agent; abnormal uterine bleeding; abnormal pregnancy; trophoblastic disease; ectopic pregnancy; molar pregnancy; human chorionic gonadotropin; hCG; abortion; gynaecological; cytostatic; abortifacient; contraceptive; gene; ss.

XX Gallus gallus.

XX Key Location/Qualifiers

XX CDS 1..30

XX /*tag= a

XX /product= "Chicken GnRH decapeptide"

XX /transl_except= (pos:1..3, aa:p-Glu)

XX /note= "This translational exception occurs when decoding the GnRH peptides shown as SEQ ID NO: 2 in claim 4, 1 and page 18 of the specification (AAE28135, AAE28137 and AAE28138 respectively)"

XX /transl_except= (pos:16..18, aa:D-Arg)

XX /note= "This translational exception occurs only when decoding the GnRH peptides shown as SEQ ID NO: 2 in claim 1 and page 18 of the specification (AAE28135 and AAE28138 respectively)"

XX /transl_except= (pos:16..18, aa:Xaa)

XX /note= "Xaa corresponds to D-Arg; This translational exception occurs only when decoding the GnRH peptide shown as SEQ ID NO: 2 in claim 1 of the specification (AAE28137)"

XX /transl_except= (pos:28..30, aa:Xaa)

XX /note= "Xaa corresponds to aza-Gly; This translational exception occurs only when decoding the GnRH peptides shown as SEQ ID NO: 2 in claim 4 and claim 1 of the specification (AAE28135 and AAE28137); CDS does not include start and stop codon"

XX /partial

XX US2002065226-A1.

XX 30-MAY-2002.

XX 28-AUG-2001; 2001US-0941094.

XX 15-OCT-1999; 99US-0419161.

XX (SILE/) SILER-KHODR T.

XX Siler-Khodr T;

XX WPI; 2002-681323/73.

XX P-PSDB; AAE28135, AAE28137, AAE28138.

XX Novel non-mammalian gonadotropin releasing hormone analogs useful to regulate reproductive functions and disorders, as menses regulators, contraceptives or abortifacients

XX Claim 15; Page 19; 57pp; English.

XX The present invention relates to novel non-mammalian peptide hormone analogues of gonadotropin releasing hormone (GnRH) capable of binding to ovarian, tubal, endometrial, uterine, prostate or testicular GnRH receptors and active in the presence of a post-proline peptidase or an endopeptidase. Sequences of the invention are useful for regulating and treating a condition of the ovaries, fallopian tubes, uterus, prostate, endometrium, testicles or tissues of pregnancy in a patient or animal. They are useful in various treatment methods as a contraceptive or post-coital contraceptive agent, for maintaining pregnancy when used in very low doses and administered in pulsatile fashion. GnRH analogues of the invention are useful in the preparations for the treatment of ovarian cysts, endometriosis and leiomyomas. They are useful as luteolytic agents in fertility regulation, as menses-inducing agents and the management of ovarian cyst, polycystic ovarian disease, abnormal uterine bleeding, in vitro fertilisation protocols, abnormal pregnancies, ectopic pregnancies, molar pregnancies and trophoblastic disease. Sequences of the invention

CC hypertension. This information can be used to find the precise role of a
 CC polymorphism in the disease, and this can be used to identify potential
 CC drugs which combat the disease. The polymorphisms can be tested for
 CC association with other diseases e.g. agammaglobulinemia, diabetes
 CC insipidus, Leech-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
 CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
 CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
 CC tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial
 CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
 CC acute intermittent porphyria. The polymorphic forms can also be used in
 CC forensics to identify individuals.

XX
 SQ Sequence 29 BP; 3 A; 8 C; 5 G; 12 T; 1 other;

Query Match 11.8%; Score 16.4; DB 21; Length 29;
 Best Local Similarity 71.4%; Pred. No. 7.1e+04;
 Matches 20; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 11 TGTAGCAGAGGCAAGCAGCAGGCTCAC 38
 DB 28 TGAAGAAGAGGCTGACACGACTTAC 1

RESULT 20

ACC46916/c
 ID ACC46916 standard; DNA; 30 BP.

AC ACC46916;

DT 05-JUN-2003 (first entry)

XX Mouse phospholipase A2 group IIA probe SEQ ID NO:13.

XX Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
 KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
 KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
 KW psoriasis; diabetes; probe; ss.

XX Mus musculus.

OS Synthetic.

XX WO200297133-A1.

XX 05-DEC-2002.

XX 21-MAY-2002; 2002WO-US16135.

XX 25-MAY-2001; 2001US-0865866.

PA (ISIS-) ISIS PHARM INC.

XX Bennett CF, Wyatt JR;

XX WPI; 2003-140495/13.

XX New compound that hybridizes with and inhibits the expression of
 PT Phospholipase A2, group IIA, useful for preparing a composition for
 PT treating or preventing inflammation, cancer, psoriasis or diabetes -
 XX Example 13; Page 84; 135pp; English.

XX The present invention describes a compound (I) comprising 8-50
 CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,
 CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
 CC A2, group IIA (synovial), where the compound specifically hybridizes with
 CC and inhibits the expression of phospholipase A2, group IIA (synovial).
 CC Also described: (1) a composition comprising the compound and a carrier
 CC or diluent; (2) a method of inhibiting the expression of phospholipase
 CC A2, group IIA in cells or tissues; and (3) a method of treating an
 CC animal having a disease or condition associated with phospholipase A2,
 CC group IIA (synovial). (I) has antiinflammatory, antidiabetic, cytostatic
 CC and antipsoriatic activities, and can be used in vaccines and in gene
 CC therapy. The compound (I) can be used for preparing a composition for

CC treating or preventing inflammation, cancer, psoriasis or diabetes. The
 CC present sequence represents a probe for mouse phospholipase A2 group IIA
 CC (synovial), which is used in an example from the present invention.

SQ Sequence 30 BP; 4 A; 11 C; 3 G; 12 T; 0 other;

Query Match 11.8%; Score 16.4; DB 25; Length 30;
 Best Local Similarity 76.9%; Pred. No. 7.1e+04;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 87 GTACGGAGATGGAGATTGGCTCCAA 112
 DB 28 GTACGAAGAGGAAGTTGGATGCCAA 3

RESULT 21

AAV52705
 ID AAV52705 standard; DNA; 22 BP.

AC AAV52705;

XX 21-DEC-1998 (first entry)

XX Hepatocyte nuclear factor 1 beta gene exon 4-2 forward PCR primer.

XX Hepatocyte nuclear factor 1 beta; HNF-1 beta; MODY4; human;
 KW transcription factor; maturity onset diabetes of the young; TCF2;
 KW diabetes; NIDDM; diagnosis; therapy; PCR; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9811254-A1.

XX 19-MAR-1998.

XX 10-SEP-1997; 97WO-US16037.

XX 30-OCT-1996; 96US-0029679.

PR 10-SEP-1996; 96US-0025719.

PR 02-OCT-1996; 96US-0028056.

XX (ARCH-) ARCH DEV CORP.

XX Bell GI, Furuta H, Horikawa Y, Kaisaki PJ, Menzel S;

XX Oda N, Yamagata K;

XX WPI; 1998-271667/24.

XX Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and
 PT 1-beta - useful for detecting susceptibility for non-insulin
 PT dependent diabetes, especially maturity-onset diabetes of the young

XX Example 8; Page 146; 363pp; English.

XX This is a forward PCR primer designed for use with a reverse primer
 CC (see AAV52706) in the PCR amplification of the 4-2 exon of the human
 CC hepatocyte nuclear factor-1 beta (HNF-1 beta) TCF2 gene (see
 CC AAV52730). Mutations of the HNF-1 beta gene have been identified by
 CC amplifying (see AAV52693-716) and sequencing the appropriate exon.
 CC The invention concerns the identification of genes responsible for
 CC non-insulin dependent diabetes mellitus (NIDDM) for use in
 CC diagnostics and therapeutics. It demonstrates that the MODY4
 CC (maturity-onset diabetes of the young) locus is the HNF-1 beta
 CC gene. Analysis of mutations in the HNF-1 beta gene can be
 CC diagnostic for diabetes.

SQ Sequence 22 BP; 8 A; 9 C; 3 G; 2 T; 0 other;

Query Match 11.7%; Score 16.2; DB 19; Length 22;
 Best Local Similarity 85.7%; Pred. No. 7.7e+04;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 28 ACCAGGCTCAGCTGGAACC 48
 |||||
 Db 2 ACCAGACTCAGGCTGAACC 22
 |||||
 RESULT 22
 AAX56275/c
 ID AAX56275 standard; DNA; 28 BP.
 XX
 AC AAX56275;
 XX
 DT 20-JUL-1999 (first entry)
 XX
 DE Human neuronal apoptosis inhibiting protein PCR primer #2.
 XX
 KW Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;
 KW spinal muscular atrophy; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN JP11116599-A.
 XX
 PD 27-APR-1999.
 XX
 PF 14-OCT-1997; 97JP-0280831.
 XX
 PR 14-OCT-1997; 97JP-0280831.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 1999-323531/27.
 XX
 PT New apoptosis inhibitory protein - useful for determining mechanism
 PT of various apoptotic diseases e.g. human spinal muscular atrophy
 XX
 PS Example 1; Page 15; 16pp; Japanese.
 XX
 CC The present sequence represents a PCR primer for human neuronal
 CC apoptosis inhibitory protein (NAIP). The apoptosis inhibitory protein
 CC is useful for the elucidation of the mechanism of various apoptosis
 CC diseases such as human spinal muscular atrophy and the diagnosis, the
 CC prevention and the treatment of such diseases.
 XX
 SQ Sequence 28 BP; 8 A; 8 C; 5 G; 7 T; 0 other;
 Query Match 11.7%; Score 16.2; DB 20; Length 28;
 Best Local Similarity 85.7%; Pred. No. 8.1e+04;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 62 CAGCGTGGTGAAGTTGGGTT 82
 |||||
 Db 25 CAGCGTGGTGAAGTTGAATT 5
 |||||
 RESULT 23
 AAT60157/c
 ID AAT60157 standard; DNA; 30 BP.
 XX
 AC AAT60157;
 XX
 DT 01-DEC-1997 (first entry)
 XX
 DE Collagen gene promoter region binding oligomer Oligo Col TFOa.
 XX
 KW Triplex; inhibition; collagen gene; promoter; pathological fibrosis;
 KW myocardial fibrosis; hypertensive heart disease; atherosclerosis;
 KW restenosis; liver cirrhosis; lung fibrosis; skin fibrosis; scleroderma;
 KW hypertrophic scar; burn injury; rat; polypurine; polypyrimidine; ss.
 XX
 OS Synthetic.
 OS WO9710254-A1.
 PN

XX 20-MAR-1997.
 PD
 XX 12-SEP-1996; 96WO-US14640.
 PF
 XX 11-SEP-1996; 96US-0712357.
 PR
 XX 15-SEP-1995; 95US-0528836.
 PR
 XX (GUNT/) GUNTAKA R V.
 PA
 XX Guntaka RV, Kandala J, Kovacs A, Weber KT;
 PI WPI; 1997-202172/18.
 XX
 DE Triplex forming oligomer binds to collagen gene promoter region -
 DE used to impede pathological fibrosis etc.
 XX
 PS Claim 18; Page 33; 52pp; English.
 XX
 CC An oligomer has been produced which is capable of inhibiting expression
 CC of a collagen gene. The present sequence represents a specifically
 CC claimed oligomer Oligo Col TFOa, which binds to the polypurine-
 CC polypyrimidine region of the rat alpha1(I) collagen gene promoter
 CC region. The oligomer may be used to impede pathological fibrosis which
 CC is associated with myocardial fibrosis in hypertensive heart diseases,
 CC atherosclerosis, restenosis, liver cirrhosis, lung fibrosis, and skin
 CC fibrosis found in scleroderma, in hypertrophic scars and in skin
 CC following burn injury. The oligomer inhibits expression of a collagen
 CC gene after insertion into a cell by causing an intracellular reaction
 CC which inhibits gene expression. The oligomer is preferably a triplex
 CC forming oligomer (TFO) which is targeted to a 30-mer polypurine
 CC oligonucleotide corresponding to the noncoding strand of the promoter
 CC between -170 and -140. This section was chosen due to its binding
 CC stability at physiological pH.
 XX
 SQ Sequence 30 BP; 11 A; 0 C; 19 G; 0 U; 0 other;
 Query Match 11.7%; Score 16.2; DB 18; Length 30;
 Best Local Similarity 85.7%; Pred. No. 8.3e+04;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 106 CTCCCAACTCTCCCTATCCT 126
 |||||
 Db 30 CTCCCACTCTCTCTCTCTCT 10
 |||||
 RESULT 24
 AAZ98705/c
 ID AAZ98705 standard; DNA; 30 BP.
 XX
 AC AAZ98705;
 XX
 DT 20-JUN-2000 (first entry)
 XX
 DE Collagen promoter inhibitory oligonucleotide Oligo Col TFOa.
 XX
 KW Collagen; inhibit; myocardial fibrosis; hypertensive heart disease;
 KW atherosclerosis; restenosis; liver cirrhosis; lung fibrosis; burn injury;
 KW peritoneal fibrosis; skin fibrosis; scleroderma; hypertrophic scar; ss.
 XX
 OS Rattus sp.
 OS WO200008213-A1.
 PN
 XX 17-FEB-2000.
 PD
 XX 06-AUG-1999; 99WO-US17824.
 PF
 XX 07-AUG-1998; 98US-0130888.
 PR
 XX (GUNT/) GUNTAKA R V.
 PA
 XX Guntaka RV, Weber KT, Kovacs A, Kandala J;
 PI


```
XX DR WPI; 2000-205739/18.
XX PT Inhibitors of collagen gene useful for treating fibrosis associated
XX FT with atherosclerosis, restenosis, liver cirrhosis, lung and skin
XX PT fibrosis, comprises oligomers capable of inhibiting collagen gene
XX PS Claim 19; Fig 1; 77pp; English.
XX CC This sequence represents an oligomer which is capable of inhibiting the
XX CC expression of the collagen gene. The oligomer is capable of binding to
XX CC the promoter region of the collagen gene. Collagen is a family of fibrous
XX CC proteins, and is the major element of skin, bone, tendon, cartilage,
XX CC blood vessels and teeth. The oligomers are useful for inhibiting
XX CC expression of the collagen gene, comprising inserting the oligomers into
XX CC a cell and causing an intracellular reaction to inhibit the gene
XX CC expression. The collagen inhibitory oligomers of the invention are useful
XX CC for treating pathological fibrosis associated with myocardial fibrosis in
XX CC hypertensive heart disease, atherosclerosis, restenosis, liver cirrhosis,
XX CC lung fibrosis, peritoneal fibrosis and skin fibrosis found in
XX CC scleroderma, hypertrophic scars and burn injury.
XX SQ Sequence 30 BP; 11 A; 0 C; 19 G; 0 U; 0 other;
    Query Match      11.7%; Score 16.2; DB 21; Length 30;
    Best Local Similarity 85.7%; Pred. No. 8.3e+04;
    Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 106 CTCGCCACTCTCCCTATCCT 126
Db 30 CTCGCCCTCTCCCTTCCT 10
RESULT 25
AAZ27655
ID RAZ27655 standard; DNA; 25 BP.
XX AC AAZ27655;
XX DT 20-DEC-1999. (first entry)
XX DE HBV genomic DNA fragment.
XX KW HBV; PCR primer; detection; infection; hepatitis B cancer; cancer marker;
XX KW therapy; ss.
XX OS Synthetic.
XX OS Hepatitis b virus.
XX PN JF11262399-A.
XX PD 28-SEP-1999.
XX PF 17-MAR-1998; 98JP-0087977.
XX PR 17-MAR-1998; 98JP-0087977.
XX PA (SRLS-) SRL KK.
XX WPI; 1999-603804/52.
XX New primer - useful for detection of hepatitis B virus
XX Example 2; Page 8; 8pp; Japanese.
XX This sequence represents a hepatitis b virus (HBV) genomic fragment,
XX CC which can be used as the primer of the invention for detecting HBV. The
XX CC primer can be used in a method for the prevention of HBV infection in
XX CC transplantation of living organism. The primer provides for highly
XX CC sensitive and specific detection of HBV without amplification of human
XX CC derived DNA. The positive ratio was 67% for detection of hepatitis B
XX CC cancer negative to HBsAg and HBeAg, and 26.1% for chronic hepatitis B.
XX CC The method is expected to be useful as a cancer marker for patients with
```

```
CC hepatitis B.
XX SQ Sequence 25 BP; 1 A; 7 C; 6 G; 9 T; 2 other;
    Query Match      11.5%; Score 16; DB 20; Length 25;
    Best Local Similarity 80.0%; Pred. No. 9.2e+04;
    Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 42 TGGAACCCCTGGTGTCTCTC 61
Db 5 TGGACCTTGTGKCTCTC 24
Search completed: August 22, 2003, 10:09:51
Job time : 209 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 10:09:59 ; Search time 47 Seconds
(without alignments)

```

Title: US-09-925-139-3_COPY_1631_1769
Perfect score: 139
Sequence: 1 cgaatggagccttatgcacaaa
          ctatccttaaaagggggagctac 139

```

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters:

Minimum DB	seq	length: 0
Maximum DB	seq	length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100%

```
Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	18	12.9	18	1	US-08-363-240A-1125	Sequence 1125, Ap	
2	16.8	12.1	27	2	US-08-558-823-11	Sequence 11, Appl	
3	16.8	12.1	30	4	US-09-419-161-1	Sequence 1, Appl	
c 4	16.4	11.8	29	3	US-09-304-233-439	Sequence 439, App	
5	16.2	11.7	22	3	US-08-927-219-102	Sequence 102, App	
c 6	16.2	11.7	30	1	US-08-802-547-6	Sequence 6, Appl	
c 7	16.2	11.7	30	1	US-08-712-357-6	Sequence 6, Appl	
c 8	15.6	11.2	30	1	US-08-458-686-7	Sequence 7, Appl	
c 9	15.6	11.2	30	1	US-08-458-686-7	Sequence 7, Appl	
c 10	15.6	11.2	30	1	US-07-843-350C-7	Sequence 7, Appl	
c 11	15.6	11.2	30	5	PTC-US93-01559-7	Sequence 7, Appl	
12	15.2	10.9	23	3	US-09-161-466-19	Sequence 19, Appl	
13	15.2	10.9	30	3	US-08-946-138-24	Sequence 24, Appl	
14	15.2	10.9	30	3	US-09-130-546D-24	Sequence 24, Appl	
15	15.2	10.9	30	4	US-09-227-694B-24	Sequence 24, Appl	
16	15.2	10.9	30	4	US-09-446-081-26	Sequence 26, Appl	
17	15	10.8	15	1	US-08-363-240A-240	Sequence 240, App	
18	15	10.8	15	1	US-08-363-240A-241	Sequence 241, App	
19	15	10.8	15	1	US-08-363-240A-241	Sequence 241, App	
20	15	10.8	15	1	US-08-363-240A-242	Sequence 242, App	
21	15	10.8	15	1	US-08-363-240A-243	Sequence 243, App	
22	15	10.8	15	1	US-08-363-240A-244	Sequence 244, App	
23	15	10.8	15	1	US-08-363-240A-245	Sequence 245, App	
24	15	10.8	15	1	US-08-363-240A-246	Sequence 246, App	
25	15	10.8	15	1	US-08-363-240A-247	Sequence 247, App	
26	15	10.8	15	1	US-08-363-240A-248	Sequence 248, App	
27	15	10.8	15	1	US-08-363-240A-249	Sequence 249, App	
	15	10.8	15	1	US-08-363-240A-250	Sequence 250, App	

C 685 12.4 8.9 24 2 US-08-859-998-961
C 686 12.4 8.9 24 3 US-08-933-358-1
C 687 12.4 8.9 24 3 US-09-069-484-10
C 688 12.4 8.9 24 3 US-09-064-964-27
C 689 12.4 8.9 24 3 US-08-559-205-35
C 690 12.4 8.9 24 3 US-08-559-205-51
C 691 12.4 8.9 24 3 US-08-513-974B-231
C 692 12.4 8.9 24 3 US-08-513-974B-233
C 693 12.4 8.9 24 3 US-08-513-974B-234
C 694 12.4 8.9 24 3 US-09-041-090B-32
C 695 12.4 8.9 24 3 US-09-041-090B-48
C 696 12.4 8.9 24 3 US-09-135-599-5
C 697 12.4 8.9 24 4 US-09-369-744-10
C 698 12.4 8.9 24 4 US-09-225-928-961
C 699 12.4 8.9 24 4 US-09-225-201B-961
C 700 12.4 8.9 24 4 US-09-318-138-41
C 701 12.4 8.9 24 4 US-09-318-138-50
C 702 12.4 8.9 24 5 PCT-US95-03602-8
C 703 12.4 8.9 25 2 US-08-743-637B-52
C 704 12.4 8.9 25 3 US-08-526-840B-52
C 705 12.4 8.9 25 3 US-09-069-886-24
C 706 12.4 8.9 25 3 US-09-315-886C-9
C 707 12.4 8.9 25 3 US-09-180-437-288
C 708 12.4 8.9 25 4 US-09-512-342-25
C 709 12.4 8.9 25 4 US-09-617-548-4
C 710 12.4 8.9 25 4 US-09-258-133-27
C 711 12.4 8.9 26 1 US-09-471-573A-36
C 712 12.4 8.9 26 1 US-08-434-503-17
C 713 12.4 8.9 26 1 US-08-623-891-108
C 714 12.4 8.9 26 2 US-08-768-147B-12
C 715 12.4 8.9 26 2 US-08-672-814D-8
C 716 12.4 8.9 26 3 US-09-400-742-16
C 717 12.4 8.9 26 3 US-08-618-651A-16
C 718 12.4 8.9 26 3 US-09-333-696-8
C 719 12.4 8.9 26 3 US-09-107-149-13
C 720 12.4 8.9 26 3 US-08-821-827C-23
C 721 12.4 8.9 26 4 US-09-215-252-36
C 722 12.4 8.9 26 4 US-09-290-202B-23
C 723 12.4 8.9 26 4 US-09-340-861-108
C 724 12.4 8.9 26 4 US-09-634-262-108
C 725 12.4 8.9 26 4 US-09-297-269-31
C 726 12.4 8.9 26 4 US-09-282-218A-8
C 727 12.4 8.9 27 2 US-08-758-621-20
C 728 12.4 8.9 27 2 US-08-140-008A-5
C 729 12.4 8.9 27 2 US-08-460-890A-14
C 730 12.4 8.9 27 2 US-08-460-890A-15
C 731 12.4 8.9 27 3 US-08-167-641C-15
C 732 12.4 8.9 27 3 US-08-167-641C-15
C 733 12.4 8.9 27 3 US-08-460-971A-14
C 734 12.4 8.9 27 3 US-08-460-971A-15
C 735 12.4 8.9 27 3 US-09-107-858-20
C 736 12.4 8.9 27 3 US-08-462-040-14
C 737 12.4 8.9 27 3 US-08-462-040-15
C 738 12.4 8.9 27 4 US-09-311-784A-96
C 739 12.4 8.9 28 2 US-08-448-438-28
C 740 12.4 8.9 28 2 US-08-174-672D-78
C 741 12.4 8.9 28 4 US-08-981-653-7
C 742 12.4 8.9 28 4 US-08-981-653-8
C 743 12.4 8.9 28 4 US-09-165-827C-4
C 744 12.4 8.9 28 4 US-09-165-827C-8
C 745 12.4 8.9 28 4 US-08-147-696B-16
C 746 12.4 8.9 29 1 US-08-484-334-16
C 747 12.4 8.9 29 1 US-08-484-334-16
C 748 12.4 8.9 29 1 US-08-484-334-31
C 749 12.4 8.9 29 2 US-08-480-736-2
C 750 12.4 8.9 29 3 US-09-013-092-16
C 751 12.4 8.9 29 3 US-09-013-092-31
C 752 12.4 8.9 29 3 US-09-280-999-16
C 753 12.4 8.9 29 3 US-09-280-999-31
C 754 12.4 8.9 29 3 US-09-000-227A-3
C 755 12.4 8.9 29 4 US-09-304-232-303
C 756 12.4 8.9 29 4 US-09-304-232-303
C 757 12.4 8.9 29 4 US-09-304-232-303

Sequence 961, App
Sequence 1, Appl
Sequence 20, Appl
Sequence 27, Appl
Sequence 35, Appl
Sequence 51, Appl
Sequence 231, App
Sequence 233, App
Sequence 234, App
Sequence 32, Appl
Sequence 48, Appl
Sequence 5, Appl
Sequence 10, Appl
Sequence 961, App
Sequence 961, App
Sequence 41, Appl
Sequence 50, Appl
Sequence 52, Appl
Sequence 52, Appl
Sequence 24, Appl
Sequence 9, Appl
Sequence 288, App
Sequence 25, Appl
Sequence 4, Appl
Sequence 27, Appl
Sequence 36, Appl
Sequence 17, Appl
Sequence 108, App
Sequence 12, Appl
Sequence 8, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 8, Appl
Sequence 13, Appl
Sequence 23, Appl
Sequence 36, Appl
Sequence 23, Appl
Sequence 108, App
Sequence 31, Appl
Sequence 20, Appl
Sequence 5, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 20, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 96, Appl
Sequence 28, Appl
Sequence 78, Appl
Sequence 8, Appl
Sequence 11, Appl
Sequence 4, Appl
Sequence 8, Appl
Sequence 15, Appl
Sequence 31, Appl
Sequence 16, Appl
Sequence 31, Appl
Sequence 2, Appl
Sequence 16, Appl
Sequence 31, Appl
Sequence 16, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 303, App
Sequence 796, App

Sequence 16, Appl
Sequence 2, Appl
Sequence 16, Appl
Sequence 149, App
Sequence 152, App
Sequence 630, App
Sequence 26, Appl
Sequence 9, Appl
Sequence 15, Appl
Sequence 3, Appl
Sequence 18, Appl
Sequence 23, Appl
Sequence 58, Appl
Sequence 59, Appl
Sequence 60, Appl
Sequence 11, Appl
Sequence 7, Appl
Sequence 191, App
Sequence 149, App
Sequence 152, App
Sequence 11, Appl
Sequence 15, Appl
Sequence 18, Appl
Sequence 15, Appl
Sequence 9, Appl
Sequence 1709, Ap
Sequence 6, Appl
Sequence 13, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 142, App
Sequence 46, Appl
Sequence 10, Appl
Sequence 21, Appl
Sequence 111, App
Sequence 46, Appl
Sequence 49, Appl
Sequence 20, Appl
Sequence 58, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 51, Appl
Sequence 66, Appl
Sequence 51, Appl
Sequence 138, App
Sequence 5, Appl
Sequence 20, Appl
Sequence 71, Appl
Sequence 4, Appl
Sequence 46, Appl
Sequence 65, Appl
Sequence 75, Appl
Sequence 581, Ap
Sequence 4039, Ap
Sequence 12, Appl
Sequence 4, Appl
Sequence 75, Appl
Sequence 6, Appl
Sequence 46, Appl
Sequence 14, Appl
Sequence 44, Appl
Sequence 46, Appl
Sequence 46, Appl

c 977	12.2	8.8	29	2	US-08-859-998-394	Sequence 394, Appl
c 978	12.2	8.8	29	3	US-09-126-280-16	Sequence 16, Appl
c 979	12.2	8.8	29	4	US-09-225-928-394	Sequence 394, App
c 980	12.2	8.8	29	4	US-09-225-201B-394	Sequence 394, App
c 981	12.2	8.8	29	4	US-09-304-232-270	Sequence 270, App
c 982	12.2	8.8	29	4	US-09-304-232-305	Sequence 305, App
c 983	12.2	8.8	29	4	US-09-304-232-359	Sequence 359, App
c 984	12.2	8.8	29	4	US-09-304-232-433	Sequence 433, App
c 985	12.2	8.8	29	4	US-09-304-232-679	Sequence 679, App
c 986	12.2	8.8	29	4	US-09-304-232-696	Sequence 696, App
c 987	12.2	8.8	29	4	US-09-848-813-8	Sequence 8, Appl
c 988	12.2	8.8	29	5	PCT-US94-04190-10	Sequence 10, Appl
c 989	12.2	8.8	30	1	US-07-931-473B-12	Sequence 12, Appl
c 990	12.2	8.8	30	1	US-08-062-022-8	Sequence 8, Appl
c 991	12.2	8.8	30	1	US-07-714-131C-12	Sequence 12, Appl
c 992	12.2	8.8	30	1	US-08-219-012-31	Sequence 31, Appl
c 993	12.2	8.8	30	1	US-07-982-174-6	Sequence 6, Appl
c 994	12.2	8.8	30	1	US-08-495-743-8	Sequence 8, Appl
c 995	12.2	8.8	30	1	US-08-419-110-12	Sequence 12, Appl
c 996	12.2	8.8	30	1	US-08-409-442A-12	Sequence 12, Appl
c 997	12.2	8.8	30	1	US-08-499-739-8	Sequence 8, Appl
c 998	12.2	8.8	30	1	US-08-297-706-6	Sequence 6, Appl
c 999	12.2	8.8	30	1	US-08-495-741-8	Sequence 8, Appl
c 1000	12.2	8.8	30	1	US-08-475-000-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
 US-08-363-240A-1125
 ; Sequence 1125, Application US/08363240A
 ; Patent No. 5705388
 ;
 GENERAL INFORMATION:
 ;
 ; APPLICANT: Couture, Larry
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Bisgaier, Charles
 ; APPLICANT: Pope, Michael
 ;
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR
 ; TITLE OF INVENTION: PREVENTION, INHIBITION OF
 ; TITLE OF INVENTION: PROGRESSION, INHIBITION OF
 ; TITLE OF INVENTION: OF VASCULAR DISEASES
 ;
 ; NUMBER OF SEQUENCES: 1243
 ;
 CORRESPONDENCE ADDRESS:
 ; ADDRESS: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ;
 ; ZIP: 90071
 ;
 COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: Storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ;
 CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/363,240A
 ; FILING DATE: December 23, 1994
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER:
 ;
 FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 210/096
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ;
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 1125:
 ; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-1125

Query Match 12.9%; Score 18; DB 1; Length 18
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 15; Conservative 0; Indels

QY 33 GCTCACAGCTGGAAACCTT 50
   |||:|||||:|||||:
DB 1 GCTCACAGCTGGAAACCTT 18

RESULT 2
US-08-558-823-11
; Sequence 11, Application US/08558823
; Patent No. 5876994
; GENERAL INFORMATION:
; APPLICANT: Knipple, Douglas C.
; APPLICANT: Roelofs, Wendell L.
; APPLICANT: Miller, Stuart J.
; TITLE OF INVENTION: PHEROMONE DESATURASES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/558,823
; APPLICATION NUMBER: US/08/558,823
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rogalsky Esq., Peter
; REGISTRATION NUMBER: 38,601
; REFERENCE/DOCKET NUMBER: 19603/400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1634
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-558-823-11

```

31,

;; TITLE OF INVENTION: Fertility and Pregnancy
;; FILE REFERENCE: P7345.2
;; CURRENT APPLICATION NUMBER: US/09/419.161
;; CURRENT FILING DATE: 1999-10-15
;; NUMBER OF SEQ ID NOS: 4
;; SEQ ID NO 1
;; LENGTH: 30
;; TYPE: DNA
;; ORGANISM: Chicken II GnrH
US-09-419-161-1

Query Match 12.1%; Score 16.8; DB 4; Length 30;
Best Local Similarity 75.0%; Pred. No. 8.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 25 AGCACAGGCTCACAGCTGAACCTGG 52
||||| ||||| ||||| ||||| |||||
Db 2 AGCACTGGTCTCATGGCTGGTATCTGG 29

RESULT 4
US-09-304-232-439/c
; Sequence 439, Application US/09304232
; Patent No. 6525185
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/09/304.232
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: US 60/084.641
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 439
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BLAM1EX3 152
US-09-304-232-439

Query Match 11.8%; Score 16.4; DB 4; Length 29;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 20; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 11 TGTAGCAGAGGCAAGCACCAGGCTCAC 38
||||| ||||| ||||| ||||| |||||
Db 28 TGAAGAAAGGCGFAGAACCCAGACTTAC 1

RESULT 5
US-08-927-219-102
; Sequence 102, Application US/08927219
; Patent No. 6187533
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I.
; APPLICANT: Yamagata, Kazuya
; APPLICANT: Oda, Nachisha
; APPLICANT: Kaieaki, Pamela J.
; APPLICANT: Furuta, Hiroto
; APPLICANT: Horikawa, Yukio
; APPLICANT: Menzel, Stephen
; TITLE OF INVENTION: MUTATIONS IN THE DIABETES SUSCEPTIBILITY
; TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA
; TITLE OF INVENTION: AND HNF-4ALPHA
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: USA
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/927,219
;; FILING DATE: Concurrently Herewith
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/029,679
;; FILING DATE: 30-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/028,056
;; FILING DATE: 02-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/025,719
;; FILING DATE: 10-SEP-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wilson, Mark B.
;; REGISTRATION NUMBER: 37,259
;; REFERENCE/DOCKET NUMBER: ARCD:272
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 512/418-3000
;; TELEFAX: 512/474-7577
;; INFORMATION FOR SEQ ID NO: 102:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 22 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-927-219-102

Query Match 11.7%; Score 16.2; DB 3; Length 22;
Best Local Similarity 85.7%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 28 ACCAGCTCACAGCTGGAACC 48
||||| ||||| ||||| |||||
Db 2 ACCAGACTCACAGCTGAACC 22

RESULT 6
US-08-802-547-6/c
; Sequence 6, Application US/08802547
; Patent No. 5780611
; GENERAL INFORMATION:
; APPLICANT: Guntaka, Ramareddy V.
; APPLICANT: Weber, Karl T.
; APPLICANT: Kovacs, Attila
; APPLICANT: Kandala, Jagannadhachari
; TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT EXPRESSION OF
; TITLE OF INVENTION: COLLAGEN GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: MO
; COUNTRY: USA
; ZIP: 64108
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:

```

; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; POSITION IN GENOME:
; UNITS: bp
US-08-712-357-6
Query Match 11.7%; Score 16.2; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 1.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTCCCAATCTCCCTATCCT 126
Db 30 CTCCCCCCTCTCCCTTCCT 10

RESULT 8
US-08-459-489-7/c
; Sequence 7, Application US/08459489
; Patent No. 5686574
; GENERAL INFORMATION:
; APPLICANT: David D. Moore et al.
; TITLE OF INVENTION: CAR RECEPTORS AND RELATED
; TITLE OF INVENTION: MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,489
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/843,350
; FILING DATE: February 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/126001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-459-489-7
Query Match 11.2%; Score 15.6; DB 1; Length 30;
Best Local Similarity 70.0%; Pred. No. 2.1e+04;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 35 TCACAGCTGGAAACCTGGTGTCTCTCCAG 64
Db 30 TCAGGGCTGCTGTCCTCTCACCTCCAG 1

RESULT 9
US-08-458-686-7/c
; Sequence 7, Application US/08458686
; Patent No. 5710017
; GENERAL INFORMATION:

```

```

RESULT 10
US-07-843-350C-7/c
; Sequence 7, Application US/07843350C
; Patent No. 5756448
;
; GENERAL INFORMATION:
; APPLICANT: David D. Moore et al.
; TITLE OF INVENTION: CAR RECEPTORS AND RELATED
; TITLE OF INVENTION: MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 556X
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/843,350C
; FILING DATE: February 26, 1992
; CLASSIFICATION: 435

```

Query Match 11.2%; Score 15.6; DB 5; Length 30;
Best Local Similarity 70.0%; Pred. No. 2.1e+04;

TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO: 24;
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-946-138-24

Query Match 10.9%; Score 15.2; DB 3; Length 30;
Best Local Similarity 85.0%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 37 ACAGCTGGAAACCTGGTGTC 56
DB 6 ACAGCTGCATCCCTGGTGAC 25

RESULT 14
US-09-130-546D-24
Sequence 24, Application US/09130546D
Patent No. 6265163
GENERAL INFORMATION:
APPLICANT: Albrecht, Glenn
APPLICANT: Brenner, Sydney
APPLICANT: DuBridge, Robert B.
TITLE OF INVENTION: Solid phase selection of differentially expressed genes
FILE REFERENCE: 5525-0056.30
CURRENT APPLICATION NUMBER: US/09/130,546D
CURRENT FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: US 09/005,222
PRIOR FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Microsoft Word 97
SEQ ID NO 24
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Adaptor
NAME/KEY: misc feature
LOCATION: (1)-(30)
OTHER INFORMATION: n = A,T,C or G
US-09-130-546D-24

Query Match 10.9%; Score 15.2; DB 3; Length 30;
Best Local Similarity 85.0%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 37 ACAGCTGGAAACCTGGTGTC 56
DB 6 ACAGCTGCATCCCTGGTGAC 25

RESULT 15
US-09-227-694B-24
Sequence 24, Application US/09227694B
Patent No. 6511802
GENERAL INFORMATION:
APPLICANT: Albrecht, Glenn
APPLICANT: Brenner, Sydney
APPLICANT: DuBridge, Robert B.
TITLE OF INVENTION: Solid Phase Selection of Differentially Expressed Genes
FILE REFERENCE: 5525-0056.31
CURRENT APPLICATION NUMBER: US/09/227,694B
CURRENT FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: US 09/130,546
PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: US 09/005,222
PRIOR FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Word 97
SEQ ID NO 24

TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO: 24;
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-946-138-24

Query Match 10.9%; Score 15.2; DB 3; Length 23;
Best Local Similarity 85.0%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 83 AGGAGTACGAGATGGAGAT 102
DB 4 AGGAGGAGGAGATGGACAT 23

RESULT 13
US-08-946-138-24
Sequence 24, Application US/08946138
Patent No. 6013445
GENERAL INFORMATION:
APPLICANT: Glenn Albrecht, Sydney Brenner, David H. Lloyd
TITLE OF INVENTION: Massively Parallel Signature Sequencing by
TITLE OF INVENTION: Ligation of Encoded Adaptors
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics, Inc.
STREET: 3832 Bay Center Place
CITY: Hayward
STATE: California
COUNTRY: USA
ZIP: 94545
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,138
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/689,587
FILING DATE: 12-AUG-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/659,453
FILING DATE: 06-JUN-96
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevitz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 808-lus
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 670-9365

TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO: 24;
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-946-138-24

Query Match 10.9%; Score 15.2; DB 3; Length 23;
Best Local Similarity 85.0%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 83 AGGAGTACGAGATGGAGAT 102
DB 4 AGGAGGAGGAGATGGACAT 23

RESULT 13
US-08-946-138-24
Sequence 24, Application US/08946138
Patent No. 6013445
GENERAL INFORMATION:
APPLICANT: Glenn Albrecht, Sydney Brenner, David H. Lloyd
TITLE OF INVENTION: Massively Parallel Signature Sequencing by
TITLE OF INVENTION: Ligation of Encoded Adaptors
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevitz, Lynx Therapeutics, Inc.
STREET: 3832 Bay Center Place
CITY: Hayward
STATE: California
COUNTRY: USA
ZIP: 94545
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,138
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/689,587
FILING DATE: 12-AUG-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/659,453
FILING DATE: 06-JUN-96
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevitz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 808-lus
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 670-9365

```
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Adaptor
; NAME/KEY: misc_feature
; LOCATION: (1)...(30)
; OTHER INFORMATION: n = A,T,C or G
US-09-227-694B-24

Query Match          10.9%; Score 15.2; DB 4; Length 30;
Best Local Similarity 85.0%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      37 ACAGCTGGAACCCCTGGTGC 56
        |||||
Db       6 ACAGCTGCATCCCTGGTGAC 25

RESULT 16
US-09-446-081-26
; Sequence 26, Application US/09446081
; Patent No. 6518023
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; TITLE OF INVENTION: High resolution physical maps of genomic DNA
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/446,081
; FILING DATE: 27-Mar-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/884,189
; FILING DATE: 27-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent M. Powers
; REGISTRATION NUMBER: 36,246
; REFERENCE/DOCKET NUMBER: 5525-0036.41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-0880
; TELEFAX: (650) 324-0960
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-446-081-26

Query Match          10.9%; Score 15.2; DB 4; Length 30;
Best Local Similarity 85.0%; Pred. No. 2.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      37 ACAGCTGGAACCCCTGGTGC 56
        |||||
Db       6 ACAGCTGCATCCCTGGTGAC 25

RESULT 17
US-08-363-240A-240
```

```
; Sequence 240, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaler, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 240:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-240

Query Match          10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2.7e+04;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      4 TGGGGCTTGACG 18
        :|||:|:|:|:|
Db       1 UGGGGCUUGACG 15

RESULT 18
US-08-363-240A-241
; Sequence 241, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaler, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
```

STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/363,240A
 FILING DATE: December 23, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 210/096
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 241:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-363-240A-241

Query Match 10.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 2.7e+04;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCGTGTAGCAGGAG 21
 Db 1 GCGUUGAGCGAG 15

RESULT 19
 US-08-363-240A-242
 Sequence 242, Application US/08363240A
 Patent No. 5705388
 GENERAL INFORMATION:
 APPLICANT: Couture, Larry
 APPLICANT: McSwiggen, James
 APPLICANT: Bisgaier, Charles
 APPLICANT: Pape, Michael
 TITLE OF INVENTION: METHOD AND REAGENT FOR
 TITLE OF INVENTION: PREVENTION, INHIBITION OF
 TITLE OF INVENTION: PROGRESSION AND REGRESSION
 TITLE OF INVENTION: OF VASCULAR DISEASES
 NUMBER OF SEQUENCES: 1243
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/363,240A

FILING DATE: December 23, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 210/096
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 242:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-363-240A-242

Query Match 10.8%; Score 15; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 2.7e+04;
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 29 CCAGGCTCACAGCTG 43
 Db 1 CCAGGCUCACAGCUG 15

RESULT 20
 US-08-363-240A-243
 Sequence 243, Application US/08363240A
 Patent No. 5705388
 GENERAL INFORMATION:
 APPLICANT: Couture, Larry
 APPLICANT: McSwiggen, James
 APPLICANT: Bisgaier, Charles
 APPLICANT: Pape, Michael
 TITLE OF INVENTION: METHOD AND REAGENT FOR
 TITLE OF INVENTION: PREVENTION, INHIBITION OF
 TITLE OF INVENTION: PROGRESSION AND REGRESSION
 TITLE OF INVENTION: OF VASCULAR DISEASES
 NUMBER OF SEQUENCES: 1243
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/363,240A
 FILING DATE: December 23, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 210/096
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 243:
 SEQUENCE CHARACTERISTICS:

```

; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-243

```

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 66.7%;
Pred. No. 2.7e+04;
Matches 10; Conservative 5; Mismatches 0; Indels

Qy 49 CTGGTGTCTCCTCCA 63
|:|:|:|:|:|:|:
Db 1 CUGGUGUCUCCUCCA 15

RESULT 21
US-08-363-240A-244
; Sequence 244, Application US/08363240A
; Patent No. 5705388

GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Bisgaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR PREVENTION, INHIBITION OF PROGRESSION AND REGRESSION OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

```
,
,
, ZIP: 90071
,
, COMPUTER READABLE FORM:
, MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
, MEDIUM TYPE: Storage
, COMPUTER: IBM Compatible
, OPERATING SYSTEM: IBM P.C. DOS 5.0
, SOFTWARE: Word Perfect 5.1
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/363,240A
, FILING DATE: December 23, 1994
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER:
```

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 21
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 244:

```

; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-244

```

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2.7e+04;
Matches 11; Conservative 4; Mismatches 0; Indels

Qy 51 GGTGTCTCTCCAGC 65
||:|:|:|:|:|
Db 1 GGUGUCUCCUCCAGC 15

RESULT 22
US-08-363-240A-245
Sequence 245, Application US/08363240A
Patent No. 5705388
GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Bisgaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
PREVENTION, INHIBITION OF
PROGRESSION AND REGRESSION
OF VASCULAR DISEASES
TITLE OF INVENTION: PREVENTION, INHIBITION OF
PROGRESSION AND REGRESSION
OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:

ADDRESSES: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

```

?
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
? MEDIUM TYPE: storage
? MEDIUM TYPE:
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: IBM P.C. DOS 5.0
? SOFTWARE: Word Perfect 5.1
?
?

```

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENCY INFORMATION
NAME: Warburg, Richard
REGISTRATION NUMBER: 32.

REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510

```

; INFORMATION FOR SEQ ID NO:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 15 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;

```

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2.7e+04;
Matches 11; Conservative 4; Mismatches 0; Indels

Qy 54 GTCCTCTCCAGCGTG 68
Db 1 GUCUCCUCCAGCGUG 15

RESULT 23
US-08-363-240A-246
; Sequence 246, Application US/08363240A
; Patent No. 5705388

```

/ /
/ / GENERAL INFORMATION:
/ /
/ / APPLICANT: Couture, Larry
/ / APPLICANT: McSwiggen, James
/ / APPLICANT: Bisgaier, Charles
/ / APPLICANT: Pape, Michael
/ /
/ / TITLE OF INVENTION: METHOD AND REAGENT FOR
/ / TITLE OF INVENTION: PREVENTION, INHIBITION OF
/ / TITLE OF INVENTION: PROGRESSION AND REGRESSION
/ / TITLE OF INVENTION: OF VASCULAR DISEASES
/ /
/ /

```


NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 246:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-246

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.7e+04;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 70 TCGAAGTTGGGTTAG 84
:||||:||||:|
Db 1 UGGAAGUUGGUAG 15

RESULT 24
US-08-363-240A-247
; Sequence 247, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-247

Query Match 10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.7e+04;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 75 GTTGGTTAGGAGTA 89
:||||:||||:|
Db 1 GUUGGUAGGUA 15

RESULT 25
US-08-363-240A-248
; Sequence 248, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

```

;
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-248

```

```

Query Match      10.8%; Score 15; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. NO. 2.7e+04;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 76 TTGGTTAGGAGTAC 90
Db 1 UUGGGUAGGAGUAC 15

```

```

Search completed: August 22, 2003, 11:46:22
Job time : 81 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 CompuGen Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: August 22, 2003, 10:00:49 ; Search time 125 Seconds
 (without alignments)
 2499.958 Million cell updates/sec

Title: US-09-925-139-3_COPY_1631_1769
 Perfect score: 139
 Sequence: 1 ggatggggcttgtagcagaa.....ctatcctaaagccactgg 139

Scoring table: IDENTITY NUC
 Gapop 10.0, Gapext 1.0

Searched: 1517243 seqs, 112408182 residues

Total number of hits satisfying chosen parameters: 787068

Minimum DB seq length: 0
 Maximum DB seq length: 30

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published Applications NA:
 1: /cgm2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
 2: /cgm2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
 3: /cgm2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
 4: /cgm2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
 5: /cgm2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
 6: /cgm2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
 7: /cgm2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
 8: /cgm2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
 9: /cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
 10: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
 11: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
 12: /cgm2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
 13: /cgm2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
 14: /cgm2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
 15: /cgm2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
 16: /cgm2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
 17: /cgm2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	14.4	20	11	US-09-802-640-52
C 2	20	14.4	20	11	US-09-925-139-5
C 3	20	14.4	20	11	US-09-925-139-5
C 4	20	14.4	20	11	US-09-925-139-28
C 5	20	14.4	20	11	US-09-925-139-29
C 6	20	14.4	20	11	US-09-925-139-30
C 7	20	14.4	20	11	US-09-925-139-47
C 8	20	14.4	20	11	US-09-925-139-48
C 9	20	14.4	20	11	US-09-925-139-49
C 10	16.8	12.1	30	9	US-09-941-094A-1
C 11	16.4	11.8	30	11	US-09-865-866-13
C 12	15.4	11.1	25	14	US-10-098-2638-15079
C 13	15.2	10.9	25	14	US-10-098-2638-15079
C 14	15.2	10.9	30	9	US-09-908-131-18
C 15	15.2	10.9	30	9	US-09-908-131-18
C 16	15.2	10.9	30	10	US-09-907-795-18

C 17	15.2	10.9	30	14	US-10-124-884-18
C 18	15	10.8	25	14	US-10-098-2638-4644
C 19	15	10.8	25	14	US-10-098-2638-108698
C 20	15	10.8	25	14	US-10-098-2638-111973
C 21	15	10.8	25	14	US-10-098-2638-121355
C 22	15	10.8	29	10	US-09-923-246-31
C 23	15	10.8	29	10	US-09-825-561A-22
C 24	15	10.8	29	12	US-10-243-072-43
C 25	15	10.8	29	14	US-10-295-723-31
C 26	14.8	10.6	20	14	US-10-005-956-1205
C 27	14.8	10.6	25	11	US-09-754-853A-628
C 28	14.8	10.6	25	14	US-10-098-2638-62267
C 29	14.8	10.6	25	14	US-10-098-2638-62895
C 30	14.6	10.5	21	11	US-09-382-860-231
C 31	14.6	10.5	24	9	US-09-853-688-47
C 32	14.6	10.5	24	9	US-09-853-688-54
C 33	14.6	10.5	25	14	US-10-098-2638-87839
C 34	14.6	10.5	25	14	US-10-098-2638-103871
C 35	14.6	10.5	30	11	US-09-997-908A-27
C 36	14.4	10.4	17	11	US-09-827-395A-480
C 37	14.4	10.4	17	11	US-09-827-395A-481
C 38	14.4	10.4	21	11	US-09-770-107-60
C 39	14.4	10.4	24	10	US-09-976-736-38
C 40	14.4	10.4	24	10	US-09-976-736-41
C 41	14.4	10.4	24	11	US-09-291-417-35
C 42	14.4	10.4	24	11	US-09-940-185-842
C 43	14.4	10.4	24	14	US-10-309-437-17
C 44	14.4	10.4	25	9	US-09-866-108-11282
C 45	14.4	10.4	25	9	US-09-866-108-11283
C 46	14.4	10.4	25	11	US-09-946-374-175
C 47	14.4	10.4	25	12	US-10-015-387A-175
C 48	14.4	10.4	25	12	US-10-006-130A-175
C 49	14.4	10.4	25	12	US-10-006-172A-175
C 50	14.4	10.4	25	14	US-10-006-856A-175
C 51	14.4	10.4	25	14	US-10-015-393A-175
C 52	14.4	10.4	25	14	US-10-015-869A-175
C 53	14.4	10.4	25	14	US-10-012-121A-175
C 54	14.4	10.4	25	14	US-10-006-116A-175
C 55	14.4	10.4	25	14	US-10-006-117A-175
C 56	14.4	10.4	25	14	US-10-017-527A-175
C 57	14.4	10.4	25	14	US-10-013-913A-175
C 58	14.4	10.4	25	14	US-10-007-194A-175
C 59	14.4	10.4	25	14	US-10-013-430A-175
C 60	14.4	10.4	25	14	US-10-011-671A-175
C 61	14.4	10.4	25	14	US-10-012-755A-175
C 62	14.4	10.4	25	14	US-10-015-386A-175
C 63	14.4	10.4	25	14	US-10-098-2638-1639
C 64	14.4	10.4	25	14	US-10-098-2638-1640
C 65	14.4	10.4	25	14	US-10-098-2638-64260
C 66	14.4	10.4	25	14	US-10-098-2638-123925
C 67	14.4	10.4	25	14	US-10-006-768A-175
C 68	14.4	10.4	25	14	US-10-017-610A-175
C 69	14.4	10.4	25	14	US-10-020-063A-175
C 70	14.4	10.4	25	14	US-10-015-391A-175
C 71	14.4	10.4	25	14	US-10-017-407A-175
C 72	14.4	10.4	25	15	US-10-006-041A-175
C 73	14.4	10.4	25	15	US-10-011-833A-175
C 74	14.4	10.4	26	15	US-10-015-822A-175
C 75	14.4	10.4	26	15	US-10-033-300-21
C 76	14.4	10.4	28	10	US-09-809-545A-79
C 77	14.4	10.4	30	15	US-10-219-935-7
C 78	14.4	10.4	20	14	US-10-238-011-39
C 79	14.4	10.4	20	14	US-10-001-076-147
C 80	14.4	10.4	20	14	US-10-105-004-109
C 81	14.2	10.2	20	14	US-10-007-078-60
C 82	14.2	10.2	20	14	US-09-798-042-82
C 83	14.2	10.2	27	9	US-09-906-419-64
C 84	14.2	10.2	28	11	US-10-003-759-9
C 85	14.2	10.2	28	13	US-10-119-136-64
C 86	14.2	10.2	28	14	US-10-302-557-13
C 87	14.2	10.2	28	14	Sequence 18, Appl
C 88	14.2	10.2	28	14	Sequence 13, Appl
C 89	14.2	10.2	28	14	Sequence 18, Appl

90	14.2	10.2	30	10	US-09-876-527-20	Sequence 20, Appl	163	13.6	9.8	25	14	US-10-098-263B-110866	Sequence 81066, A
91	14.2	10.2	30	13	US-10-139-262-35	Sequence 35, Appl	c 164	13.6	9.8	25	14	US-10-098-263B-110806	Sequence 110806, A
92	14.2	10.2	30	14	US-10-255-969-35	Sequence 35, Appl	165	13.6	9.8	25	14	US-10-098-263B-122086	Sequence 122086, A
93	14.2	10.2	30	14	US-10-148-055A-6	Sequence 6, Appl	166	13.6	9.8	25	14	US-10-098-263B-132053	Sequence 132053, A
94	14	10.1	22	12	US-10-159-006-98	Sequence 98, Appl	c 167	13.6	9.8	27	9	US-09-824-984-9	Sequence 9, Appl
95	14	10.1	23	11	US-09-371-347-7	Sequence 7, Appl	c 168	13.6	9.8	27	9	US-09-824-851-9	Sequence 9, Appl
96	14	10.1	25	10	US-09-739-707-8	Sequence 8, Appl	c 169	13.6	9.8	27	9	US-09-825-247A-9	Sequence 9, Appl
97	14	10.1	25	12	US-10-261-517-11	Sequence 11, Appl	c 170	13.6	9.8	27	9	US-09-825-247A-9	Sequence 9, Appl
98	14	10.1	25	14	US-10-215-112-2547	Sequence 2547, Ap	c 171	13.6	9.8	27	9	US-09-825-246A-9	Sequence 9, Appl
99	14	10.1	25	14	US-10-215-112-10730	Sequence 10730, A	c 172	13.6	9.8	27	9	US-09-825-246A-9	Sequence 9, Appl
100	14	10.1	25	14	US-10-098-263B-25174	Sequence 25174, A	c 173	13.6	9.8	27	9	US-09-825-246-9	Sequence 9, Appl
101	14	10.1	25	14	US-10-098-263B-34349	Sequence 34349, A	c 174	13.6	9.8	27	9	US-09-825-246-9	Sequence 9, Appl
102	14	10.1	25	14	US-10-098-263B-41965	Sequence 41965, A	c 175	13.6	9.8	28	9	US-09-825-244A-9	Sequence 9, Appl
103	14	10.1	25	14	US-10-098-263B-46376	Sequence 46376, A	c 176	13.6	9.8	28	9	US-09-825-244A-9	Sequence 9, Appl
104	14	10.1	30	9	US-09-825-901-35	Sequence 35, Appl	c 177	13.6	9.8	29	14	US-09-798-042-78	Sequence 78, Appl
105	14	10.1	30	9	US-09-736-863-46	Sequence 46, Appl	c 178	13.6	9.8	29	14	US-10-191-513A-46	Sequence 46, Appl
106	14	10.1	30	9	US-09-736-863-47	Sequence 47, Appl	c 179	13.6	9.8	30	9	US-09-941-094A-3	Sequence 3, Appl
107	14	10.1	30	9	US-09-736-863-63	Sequence 63, Appl	c 180	13.6	9.8	30	12	US-10-190-030B-22	Sequence 22, Appl
108	14	10.1	30	12	US-10-340-860A-12	Sequence 12, Appl	c 181	13.4	9.6	30	14	US-10-175-002-6	Sequence 6, Appl
109	14	10.1	30	14	US-10-147-910-31	Sequence 31, Appl	c 182	13.4	9.6	30	14	US-09-877-478-1745	Sequence 1745, Ap
110	13.8	9.9	17	11	US-09-877-478-302	Sequence 302, App	c 183	13.4	9.6	17	11	US-09-877-478-1745	Sequence 989, App
111	13.8	9.9	17	11	US-09-877-478-303	Sequence 303, App	c 184	13.4	9.6	20	14	US-10-175-223-9	Sequence 9, Appl
112	13.8	9.9	17	11	US-09-877-478-1613	Sequence 1613, Ap	c 185	13.4	9.6	24	11	US-09-951-502A-12	Sequence 12, Appl
113	13.8	9.9	17	11	US-09-877-478-2360	Sequence 2360, Ap	c 186	13.4	9.6	24	14	US-10-126-120-3	Sequence 3, Appl
114	13.8	9.9	20	14	US-10-243-035-7	Sequence 7, Appl	c 187	13.4	9.6	25	9	US-09-866-108-11281	Sequence 11281, A
115	13.8	9.9	20	14	US-10-006-911-59	Sequence 59, Appl	c 188	13.4	9.6	25	9	US-09-866-108-11286	Sequence 11285, A
116	13.8	9.9	21	10	US-09-944-326-12	Sequence 12, Appl	c 189	13.4	9.6	25	9	US-09-866-108-15100	Sequence 11286, A
117	13.8	9.9	25	9	US-09-766-399-10	Sequence 10, Appl	c 190	13.4	9.6	25	9	US-09-866-108-15101	Sequence 15100, A
118	13.8	9.9	25	9	US-09-866-108-11284	Sequence 11284, A	c 191	13.4	9.6	25	9	US-09-866-108-15101	Sequence 15101, A
119	13.8	9.9	25	14	US-10-215-112-8045	Sequence 8045, Ap	c 192	13.4	9.6	25	11	US-09-754-853A-494	Sequence 15102, A
120	13.8	9.9	25	14	US-10-098-263B-694	Sequence 694, App	c 193	13.4	9.6	25	14	US-10-060-756A-2352	Sequence 494, App
121	13.8	9.9	25	14	US-10-098-263B-694	Sequence 694, App	c 194	13.4	9.6	25	14	US-10-060-756A-2353	Sequence 2352, Ap
122	13.8	9.9	25	14	US-10-098-263B-15922	Sequence 15922, A	c 195	13.4	9.6	25	14	US-10-060-756A-2354	Sequence 2353, Ap
123	13.8	9.9	25	14	US-10-098-263B-25767	Sequence 25767, A	c 196	13.4	9.6	25	14	US-10-098-263B-4643	Sequence 2354, Ap
124	13.8	9.9	25	14	US-10-098-263B-26801	Sequence 26801, A	c 197	13.4	9.6	25	14	US-10-098-263B-12111	Sequence 4643, Ap
125	13.8	9.9	25	14	US-10-098-263B-48588	Sequence 48588, A	c 198	13.4	9.6	25	14	US-10-098-263B-14198	Sequence 12111, A
126	13.8	9.9	25	14	US-10-098-263B-50093	Sequence 50093, A	c 199	13.4	9.6	25	14	US-10-098-263B-23306	Sequence 14198, A
127	13.8	9.9	25	14	US-10-098-263B-74269	Sequence 74269, A	c 200	13.4	9.6	25	14	US-10-098-263B-27631	Sequence 23306, A
128	13.8	9.9	25	14	US-10-098-263B-91433	Sequence 91433, A	c 201	13.4	9.6	25	14	US-10-098-263B-32970	Sequence 27631, A
129	13.8	9.9	25	14	US-10-098-263B-104296	Sequence 104296, A	c 202	13.4	9.6	25	14	US-10-098-263B-34999	Sequence 32970, A
130	13.8	9.9	25	14	US-10-098-263B-116361	Sequence 116361, A	c 203	13.4	9.6	25	14	US-10-098-263B-35926	Sequence 34999, A
131	13.8	9.9	25	14	US-10-098-263B-119874	Sequence 119874, A	c 204	13.4	9.6	25	14	US-10-098-263B-36459	Sequence 35926, A
132	13.8	9.9	26	11	US-09-864-636A-1441	Sequence 1441, Ap	c 205	13.4	9.6	25	14	US-10-098-263B-42566	Sequence 36459, A
133	13.8	9.9	27	9	US-09-796-487-16	Sequence 16, Appl	c 206	13.4	9.6	25	14	US-10-098-263B-42566	Sequence 42566, A
134	13.8	9.9	27	14	US-10-005-956-1242	Sequence 1242, Ap	c 207	13.4	9.6	25	14	US-10-098-263B-49905	Sequence 42566, A
135	13.8	9.9	29	9	US-09-732-914-100	Sequence 100, App	c 208	13.4	9.6	25	14	US-10-098-263B-53211	Sequence 49905, A
136	13.8	9.9	29	14	US-10-062-458-6	Sequence 6, Appl	c 209	13.4	9.6	25	14	US-10-098-263B-96396	Sequence 53211, A
137	13.8	9.9	30	11	US-09-899-615-11	Sequence 11, Appl	c 210	13.4	9.6	25	14	US-10-098-263B-97979	Sequence 96396, A
138	13.6	9.8	20	11	US-09-784-674-587	Sequence 587, App	c 211	13.4	9.6	25	14	US-10-098-263B-108697	Sequence 97979, A
139	13.6	9.8	21	10	US-09-778-510-14	Sequence 14, Appl	c 212	13.4	9.6	25	14	US-10-098-263B-109382	Sequence 108697, A
140	13.6	9.8	21	12	US-10-302-041-14	Sequence 14, Appl	c 213	13.4	9.6	25	14	US-10-098-263B-111228	Sequence 109382, A
141	13.6	9.8	21	14	US-10-052-972-1	Sequence 1, Appl	c 214	13.4	9.6	25	14	US-10-098-263B-111974	Sequence 111228, A
142	13.6	9.8	21	14	US-10-052-972-2	Sequence 2, Appl	c 215	13.4	9.6	25	14	US-10-098-263B-116907	Sequence 111974, A
143	13.6	9.8	21	14	US-10-052-972-3	Sequence 3, Appl	c 216	13.4	9.6	25	14	US-10-098-263B-121356	Sequence 116907, A
144	13.6	9.8	21	14	US-10-213-770A-3	Sequence 3, Appl	c 217	13.4	9.6	25	14	US-10-098-263B-121875	Sequence 121356, A
145	13.6	9.8	21	14	US-10-213-770A-4	Sequence 4, Appl	c 218	13.4	9.6	25	14	US-10-098-263B-122031	Sequence 121875, A
146	13.6	9.8	21	14	US-10-213-770A-5	Sequence 5, Appl	c 219	13.4	9.6	25	14	US-10-060-998-2220	Sequence 122031, A
147	13.6	9.8	24	11	US-09-940-185-2635	Sequence 2635, Ap	c 220	13.4	9.6	25	14	US-10-060-998-2221	Sequence 2220, Ap
148	13.6	9.8	24	11	US-09-940-185-3237	Sequence 3237, Ap	c 221	13.4	9.6	25	14	US-10-060-998-2222	Sequence 2221, Ap
149	13.6	9.8	25	10	US-09-886-156-5	Sequence 5, Appl	c 222	13.4	9.6	26	11	US-09-924-981-28	Sequence 2222, Ap
150	13.6	9.8	25	10	US-09-886-150-5	Sequence 5, Appl	c 223	13.4	9.6	26	11	US-10-003-152-42	Sequence 28, Appl
151	13.6	9.8	25	11	US-09-886-149-5	Sequence 5, Appl	c 224	13.4	9.6	26	14	US-10-002-050-42	Sequence 42, Appl
152	13.6	9.8	25	11	US-09-886-159-5	Sequence 5, Appl	c 225	13.4	9.6	26	14	US-10-002-304-42	Sequence 42, Appl
153	13.6	9.8	25	11	US-09-886-159-5	Sequence 5, Appl	c 226	13.4	9.6	26	14	US-08-796-570A-8	Sequence 8, Appl
154	13.6	9.8	25	14	US-10-098-263B-9770	Sequence 10418, A	c 227	13.4	9.6	27	11	US-09-929-752-6	Sequence 6, Appl
155	13.6	9.8	25	14	US-10-098-263B-11263	Sequence 11263, A	c 228	13.4	9.6	27	12	US-10-378-087A-2	Sequence 2, Appl
156	13.6	9.8	25	14	US-10-098-263B-15080	Sequence 15080, A	c 229	13.4	9.6	27	13	US-10-044-592-21	Sequence 21, Appl
157	13.6	9.8	25	14	US-10-098-263B-31205	Sequence 31205, A	c 230	13.4	9.6	27	13	US-10-067-477-8	Sequence 8, Appl
158	13.6	9.8	25	14	US-10-098-263B-32293	Sequence 32293, A	c 231	13.4	9.6	27	13	US-10-090-569-8	Sequence 8, Appl
159	13.6	9.8	25	14	US-10-098-263B-43529	Sequence 43529, A	c 232	13.4	9.6	27	14	US-10-001-546-63	Sequence 63, Appl
160	13.6	9.8	25	14	US-10-098-263B-55621	Sequence 55621, A	c 233	13.4	9.6	27	14	US-10-184-722-6	Sequence 6, Appl
161	13.6	9.8	25	14	US-10-098-263B-63516	Sequence 63516, A	c 234	13.4	9.6	27	14	US-10-245-801-2	Sequence 2, Appl
162	13.6	9.8	25	14	US-10-098-263B-81065	Sequence 81065, A	c 235	13.4	9.6	27	14	US-10-184-426-6	Sequence 6, Appl

236	13.4	9.6	29	10	US-09-736-960-122	Sequence 122, App	C 309	13.2	9.5	26	11	US-09-990-711-242	Sequence 242, App
237	13.4	9.6	29	11	US-09-374-046A-162	Sequence 162, App	C 310	13.2	9.5	26	11	US-09-989-726-242	Sequence 242, App
238	13.4	9.6	30	10	US-09-739-088-18	Sequence 10, Appl	C 311	13.2	9.5	26	11	US-09-998-156-242	Sequence 242, App
239	13.4	9.6	30	14	US-10-136-444-28	Sequence 28, Appl	C 312	13.2	9.5	26	11	US-09-990-437-242	Sequence 242, App
240	13.4	9.6	30	14	US-10-251-385-115	Sequence 115, App	C 313	13.2	9.5	26	11	US-09-991-157-242	Sequence 242, App
241	13.4	9.6	30	14	US-10-309-851-29	Sequence 29, Appl	C 314	13.2	9.5	26	11	US-09-997-514-242	Sequence 242, App
242	13.2	9.5	29	11	US-09-972-115A-27	Sequence 27, Appl	C 315	13.2	9.5	26	11	US-09-997-573-242	Sequence 242, App
243	13.2	9.5	20	10	US-09-745-605-16	Sequence 16, Appl	C 316	13.2	9.5	26	11	US-09-991-172-242	Sequence 242, App
244	13.2	9.5	20	10	US-09-969-373-1709	Sequence 1709, App	C 317	13.2	9.5	26	11	US-09-990-726-242	Sequence 242, App
245	13.2	9.5	21	14	US-10-066-191-68	Sequence 68, Appl	C 318	13.2	9.5	26	11	US-09-997-559-242	Sequence 242, App
246	13.2	9.5	22	14	US-10-194-370-16	Sequence 16, Appl	C 319	13.2	9.5	26	11	US-09-997-601-242	Sequence 242, App
247	13.2	9.5	22	14	US-10-216-540-4	Sequence 4, Appl	C 320	13.2	9.5	26	11	US-09-997-628-242	Sequence 242, App
248	13.2	9.5	23	8	US-08-913-430-17	Sequence 17, Appl	C 321	13.2	9.5	26	11	US-09-997-683-242	Sequence 242, App
249	13.2	9.5	23	14	US-10-112-267-121	Sequence 121, App	C 322	13.2	9.5	26	11	US-09-989-729A-242	Sequence 242, App
250	13.2	9.5	24	11	US-09-854-140-6	Sequence 6, Appl	C 323	13.2	9.5	26	11	US-09-997-349-242	Sequence 242, App
251	13.2	9.5	24	11	US-09-940-185-674	Sequence 674, App	C 324	13.2	9.5	26	11	US-09-991-854-242	Sequence 242, App
252	13.2	9.5	24	11	US-09-940-185-3270	Sequence 3270, App	C 325	13.2	9.5	26	11	US-09-997-683-242	Sequence 242, App
253	13.2	9.5	24	11	US-09-940-185-3324	Sequence 3324, App	C 326	13.2	9.5	26	11	US-09-997-729A-242	Sequence 242, App
254	13.2	9.5	25	9	US-09-866-108-3457	Sequence 3457, App	C 327	13.2	9.5	26	11	US-09-997-440-242	Sequence 242, App
255	13.2	9.5	25	9	US-09-866-108-3458	Sequence 3458, App	C 328	13.2	9.5	26	11	US-09-990-440-242	Sequence 242, App
256	13.2	9.5	25	9	US-09-866-108-3459	Sequence 3459, App	C 329	13.2	9.5	26	11	US-09-993-469-242	Sequence 242, App
257	13.2	9.5	25	9	US-09-866-108-3460	Sequence 3460, App	C 330	13.2	9.5	26	11	US-09-997-542-242	Sequence 242, App
258	13.2	9.5	25	9	US-09-866-108-3461	Sequence 3461, App	C 331	13.2	9.5	26	11	US-09-993-748-242	Sequence 242, App
259	13.2	9.5	25	9	US-09-866-108-3462	Sequence 3462, App	C 332	13.2	9.5	26	11	US-09-990-439-242	Sequence 242, App
260	13.2	9.5	25	9	US-09-866-108-3463	Sequence 3463, App	C 333	13.2	9.5	26	11	US-09-990-427-242	Sequence 242, App
261	13.2	9.5	25	9	US-09-866-108-3464	Sequence 3464, App	C 334	13.2	9.5	26	11	US-09-989-328-242	Sequence 242, App
262	13.2	9.5	25	11	US-09-992-665-248	Sequence 248, App	C 335	13.2	9.5	26	11	US-09-993-583-242	Sequence 242, App
263	13.2	9.5	25	11	US-09-940-185-4640	Sequence 4640, App	C 336	13.2	9.5	26	11	US-09-941-992-242	Sequence 242, App
264	13.2	9.5	25	14	US-10-215-112-2584	Sequence 2584, App	C 337	13.2	9.5	26	11	US-09-992-521-242	Sequence 242, App
265	13.2	9.5	25	14	US-10-044-692-190	Sequence 190, App	C 338	13.2	9.5	26	11	US-09-997-333-242	Sequence 242, App
266	13.2	9.5	25	14	US-10-044-539-190	Sequence 190, App	C 339	13.2	9.5	26	11	US-09-997-384-242	Sequence 242, App
267	13.2	9.5	25	14	US-10-098-263B-4849	Sequence 4849, App	C 340	13.2	9.5	26	11	US-09-998-041-242	Sequence 242, App
268	13.2	9.5	25	14	US-10-098-263B-30183	Sequence 30183, App	C 341	13.2	9.5	26	11	US-09-997-585-242	Sequence 242, App
269	13.2	9.5	25	14	US-10-098-263B-30581	Sequence 30581, App	C 342	13.2	9.5	26	11	US-09-997-614-242	Sequence 242, App
270	13.2	9.5	25	14	US-10-098-263B-31408	Sequence 31408, App	C 343	13.2	9.5	26	11	US-09-989-862-242	Sequence 242, App
271	13.2	9.5	25	14	US-10-098-263B-31880	Sequence 31880, App	C 344	13.2	9.5	26	11	US-09-997-729-242	Sequence 242, App
272	13.2	9.5	25	14	US-10-098-263B-50958	Sequence 50958, App	C 345	13.2	9.5	26	11	US-09-997-514-242	Sequence 242, App
273	13.2	9.5	25	14	US-10-098-263B-62268	Sequence 62268, App	C 346	13.2	9.5	26	11	US-10-244-718-3	Sequence 3, Appl
274	13.2	9.5	25	14	US-10-098-263B-62896	Sequence 62896, App	C 347	13.2	9.5	26	11	US-10-005-956-1216	Sequence 1216, App
275	13.2	9.5	25	14	US-10-098-263B-79540	Sequence 79540, App	C 348	13.2	9.5	26	11	US-09-987-456-101	Sequence 101, App
276	13.2	9.5	25	14	US-10-098-263B-94552	Sequence 94552, App	C 349	13.2	9.5	26	11	US-09-818-991-55	Sequence 55, Appl
277	13.2	9.5	25	14	US-10-098-263B-113613	Sequence 113613, App	C 350	13.2	9.5	26	11	US-09-867-947-45	Sequence 45, Appl
278	13.2	9.5	25	14	US-10-098-263B-113944	Sequence 113944, App	C 351	13.2	9.5	26	11	US-10-061-395-90	Sequence 90, Appl
279	13.2	9.5	25	14	US-10-098-263B-124517	Sequence 124517, App	C 352	13.2	9.5	26	11	US-10-136-574-4	Sequence 4, Appl
280	13.2	9.5	25	14	US-09-118-276-16	Sequence 16, App	C 353	13.2	9.5	26	11	US-10-302-557-14	Sequence 14, Appl
281	13.2	9.5	26	9	US-09-989-722-242	Sequence 242, App	C 354	13.2	9.5	26	11	US-10-052-942-133	Sequence 133, Appl
282	13.2	9.5	26	9	US-09-989-723-242	Sequence 242, App	C 355	13.2	9.5	26	11	US-09-852-209A-30	Sequence 30, Appl
283	13.2	9.5	26	9	US-09-989-729-242	Sequence 242, App	C 356	13.2	9.5	26	11	US-10-146-255-4	Sequence 4, Appl
284	13.2	9.5	26	9	US-09-989-727-242	Sequence 242, App	C 357	13.2	9.5	26	11	US-10-241-476-16	Sequence 16, Appl
285	13.2	9.5	26	10	US-09-989-727-242	Sequence 242, App	C 358	13.2	9.5	26	11	US-10-085-906-203	Sequence 203, App
286	13.2	9.5	26	10	US-09-989-732-242	Sequence 242, App	C 359	13.2	9.5	26	11	US-10-131-600-30	Sequence 30, Appl
287	13.2	9.5	26	10	US-09-991-073-242	Sequence 242, App	C 360	13.2	9.5	26	11	US-09-877-478-2361	Sequence 2361, App
288	13.2	9.5	26	10	US-09-990-442-242	Sequence 242, App	C 361	13.2	9.5	26	11	US-09-983-531A-44	Sequence 44, Appl
289	13.2	9.5	26	10	US-09-991-163-242	Sequence 242, App	C 362	13.2	9.5	26	11	US-09-792-251-26	Sequence 26, Appl
290	13.2	9.5	26	10	US-09-993-604-242	Sequence 242, App	C 363	13.2	9.5	26	11	US-09-382-860-221	Sequence 221, App
291	13.2	9.5	26	10	US-09-990-456-242	Sequence 242, App	C 364	13.2	9.5	26	11	US-10-184-085A-293	Sequence 293, App
292	13.2	9.5	26	10	US-09-989-721-242	Sequence 242, App	C 365	13.2	9.5	26	11	US-10-079-429-19	Sequence 19, Appl
293	13.2	9.5	26	10	US-09-992-588-242	Sequence 242, App	C 366	13.2	9.5	26	11	US-10-071-386-32	Sequence 32, Appl
294	13.2	9.5	26	10	US-09-989-735-242	Sequence 242, App	C 367	13.2	9.5	26	11	US-09-848-990-12	Sequence 12, Appl
295	13.2	9.5	26	10	US-09-990-444-242	Sequence 242, App	C 368	13.2	9.5	26	11	US-09-924-231-4	Sequence 4, Appl
296	13.2	9.5	26	10	US-09-991-181-242	Sequence 242, App	C 369	13.2	9.5	26	11	US-09-901-484A-472	Sequence 472, App
297	13.2	9.5	26	10	US-09-989-730-242	Sequence 242, App	C 370	13.2	9.5	26	11	US-09-925-673-3	Sequence 3, Appl
298	13.2	9.5	26	10	US-09-993-687-242	Sequence 242, App	C 371	13.2	9.5	26	11	US-09-920-552-86	Sequence 86, Appl
299	13.2	9.5	26	11	US-09-989-734-242	Sequence 242, App	C 372	13.2	9.5	26	11	US-09-733-692A-12	Sequence 12, Appl
300	13.2	9.5	26	11	US-09-997-653-242	Sequence 242, App	C 373	13.2	9.5	26	11	US-09-940-185-1514	Sequence 1514, App
301	13.2	9.5	26	11	US-09-993-667-242	Sequence 242, App	C 374	13.2	9.5	26	11	US-09-940-185-1795	Sequence 1795, App
302	13.2	9.5	26	11	US-09-997-428-242	Sequence 242, App	C 375	13.2	9.5	26	11	US-09-940-185-2373	Sequence 2373, App
303	13.2	9.5	26	11	US-09-997-666-242	Sequence 242, App	C 376	13.2	9.5	26	11	US-09-940-185-3351	Sequence 3351, App
304	13.2	9.5	26	11	US-09-997-666-242	Sequence 242, App	C 377	13.2	9.5	26	11	US-10-072-094-38	Sequence 38, Appl
305	13.2	9.5	26	11	US-09-997-666-242	Sequence 242, App	C 378	13.2	9.5	26	11	US-10-141-956-19	Sequence 19, Appl
306	13.2	9.5	26	11	US-09-997-666-242	Sequence 242, App	C 379	13.2	9.5	26	11		
307	13.2	9.5	26	11	US-09-997-666-242	Sequence 242, App	C 380	13.2	9.5	26	11		
308	13.2	9.5	26	11	US-09-997-666-242	Sequence 242, App	C 381	13.2	9.5	26	11		

C 382	13	9.4	25	9	US-09-866-108-4193	Sequence 4193, Ap	455	12.8	9.2	20	11	US-09-784-674-445	Sequence 445, App
C 383	13	9.4	25	9	US-09-866-108-4194	Sequence 4194, Ap	456	12.8	9.2	20	11	US-09-906-158-78	Sequence 78, Appl
C 384	13	9.4	25	9	US-09-866-108-4195	Sequence 4195, Ap	457	12.8	9.2	21	14	US-10-093-626B-5	Sequence 5, Appl
C 385	13	9.4	25	9	US-09-866-108-4196	Sequence 4196, Ap	458	12.8	9.2	24	9	US-09-989-722-481	Sequence 481, App
C 386	13	9.4	25	9	US-09-866-108-4197	Sequence 4197, Ap	459	12.8	9.2	24	9	US-09-989-723-481	Sequence 481, App
C 387	13	9.4	25	14	US-10-215-112-5293	Sequence 5293, Ap	460	12.8	9.2	24	9	US-09-989-727-481	Sequence 481, App
C 388	13	9.4	25	14	US-10-215-112-10959	Sequence 10959, A	461	12.8	9.2	24	10	US-09-989-731-481	Sequence 481, App
C 389	13	9.4	25	14	US-10-215-112-11510	Sequence 11510, A	462	12.8	9.2	24	10	US-09-919-585-16	Sequence 16, Appl
C 390	13	9.4	25	14	US-10-098-263B-4769	Sequence 4769, Ap	463	12.8	9.2	24	10	US-09-989-732-481	Sequence 481, App
C 391	13	9.4	25	14	US-10-098-263B-6706	Sequence 6706, Ap	464	12.8	9.2	24	10	US-09-991-073-481	Sequence 481, App
C 392	13	9.4	25	14	US-10-098-263B-8201	Sequence 8201, Ap	465	12.8	9.2	24	10	US-09-990-442-481	Sequence 481, App
C 393	13	9.4	25	14	US-10-098-263B-9802	Sequence 9802, Ap	466	12.8	9.2	24	10	US-09-991-163-481	Sequence 481, App
C 394	13	9.4	25	14	US-10-098-263B-10438	Sequence 10438, A	467	12.8	9.2	24	10	US-09-993-604-481	Sequence 481, App
C 395	13	9.4	25	14	US-10-098-263B-14325	Sequence 14325, A	468	12.8	9.2	24	10	US-09-990-450-481	Sequence 481, App
C 396	13	9.4	25	14	US-10-098-263B-14326	Sequence 14326, A	469	12.8	9.2	24	10	US-09-989-721-481	Sequence 481, App
C 397	13	9.4	25	14	US-10-098-263B-14868	Sequence 14868, A	470	12.8	9.2	24	10	US-09-992-598-481	Sequence 481, App
C 398	13	9.4	25	14	US-10-098-263B-31323	Sequence 31323, A	471	12.8	9.2	24	10	US-09-989-293A-481	Sequence 481, App
C 399	13	9.4	25	14	US-10-098-263B-31324	Sequence 31324, A	472	12.8	9.2	24	10	US-09-989-735-481	Sequence 481, App
C 400	13	9.4	25	14	US-10-098-263B-38388	Sequence 38388, A	473	12.8	9.2	24	10	US-09-990-444-481	Sequence 481, App
C 401	13	9.4	25	14	US-10-098-263B-38419	Sequence 38419, A	474	12.8	9.2	24	10	US-09-991-181-481	Sequence 481, App
C 402	13	9.4	25	14	US-10-098-263B-42218	Sequence 42218, A	475	12.8	9.2	24	10	US-09-989-730-481	Sequence 481, App
C 403	13	9.4	25	14	US-10-098-263B-42888	Sequence 42888, A	476	12.8	9.2	24	10	US-09-990-436-481	Sequence 481, App
C 404	13	9.4	25	14	US-10-098-263B-47665	Sequence 47665, A	477	12.8	9.2	24	10	US-09-993-687-481	Sequence 481, App
C 405	13	9.4	25	14	US-10-098-263B-47666	Sequence 47666, A	478	12.8	9.2	24	10	US-09-989-734-481	Sequence 481, App
C 406	13	9.4	25	14	US-10-098-263B-56417	Sequence 56417, A	479	12.8	9.2	24	11	US-09-883-152-104	Sequence 104, App
C 407	13	9.4	25	14	US-10-098-263B-66712	Sequence 66712, A	480	12.8	9.2	24	11	US-09-997-653-481	Sequence 481, App
C 408	13	9.4	25	14	US-10-098-263B-68746	Sequence 68746, A	481	12.8	9.2	24	11	US-09-993-667-481	Sequence 481, App
C 409	13	9.4	25	14	US-10-098-263B-68746	Sequence 68746, A	482	12.8	9.2	24	11	US-09-997-428-481	Sequence 481, App
C 410	13	9.4	25	14	US-10-098-263B-69725	Sequence 69725, A	483	12.8	9.2	24	11	US-09-997-666-481	Sequence 481, App
C 411	13	9.4	25	14	US-10-098-263B-72977	Sequence 72977, A	484	12.8	9.2	24	11	US-09-990-438-481	Sequence 481, App
C 412	13	9.4	25	14	US-10-098-263B-72978	Sequence 72978, A	485	12.8	9.2	24	11	US-09-990-562-481	Sequence 481, App
C 413	13	9.4	25	14	US-10-098-263B-73456	Sequence 73456, A	486	12.8	9.2	24	11	US-09-990-562-481	Sequence 481, App
C 414	13	9.4	25	14	US-10-098-263B-74596	Sequence 74596, A	487	12.8	9.2	24	11	US-09-989-726-481	Sequence 481, App
C 415	13	9.4	25	14	US-10-098-263B-82540	Sequence 82540, A	488	12.8	9.2	24	11	US-09-998-156-481	Sequence 481, App
C 416	13	9.4	25	14	US-10-098-263B-85470	Sequence 85470, A	489	12.8	9.2	24	11	US-09-990-437-481	Sequence 481, App
C 417	13	9.4	25	14	US-10-098-263B-87840	Sequence 87840, A	490	12.8	9.2	24	11	US-09-991-157-481	Sequence 481, App
C 418	13	9.4	25	14	US-10-098-263B-93186	Sequence 93186, A	491	12.8	9.2	24	11	US-09-997-514-481	Sequence 481, App
C 419	13	9.4	25	14	US-10-098-263B-98907	Sequence 98907, A	492	12.8	9.2	24	11	US-09-997-573-481	Sequence 481, App
C 420	13	9.4	25	14	US-10-098-263B-100503	Sequence 100503, A	493	12.8	9.2	24	11	US-09-991-172-481	Sequence 481, App
C 421	13	9.4	25	14	US-10-098-263B-102245	Sequence 102245, A	494	12.8	9.2	24	11	US-09-990-726-481	Sequence 481, App
C 422	13	9.4	25	14	US-10-098-263B-103872	Sequence 103872, A	495	12.8	9.2	24	11	US-09-997-559-481	Sequence 481, App
C 423	13	9.4	25	14	US-10-098-263B-109385	Sequence 109385, A	496	12.8	9.2	24	11	US-09-997-601-481	Sequence 481, App
C 424	13	9.4	25	14	US-10-098-263B-110612	Sequence 110612, A	497	12.8	9.2	24	11	US-09-990-443-481	Sequence 481, App
C 425	13	9.4	25	14	US-10-098-263B-119684	Sequence 119684, A	498	12.8	9.2	24	11	US-09-991-854-481	Sequence 481, App
C 426	13	9.4	25	14	US-10-098-263B-120322	Sequence 120322, A	499	12.8	9.2	24	11	US-09-997-628-481	Sequence 481, App
C 427	13	9.4	25	14	US-10-098-263B-121395	Sequence 121395, A	500	12.8	9.2	24	11	US-09-997-683-481	Sequence 481, App
C 428	13	9.4	25	14	US-10-303-786-3	Sequence 3, Appl	501	12.8	9.2	24	11	US-09-989-729A-481	Sequence 481, App
C 429	13	9.4	26	9	US-09-796-861-1	Sequence 1, Appl	502	12.8	9.2	24	11	US-09-997-349-481	Sequence 481, App
C 430	13	9.4	26	11	US-09-770-107-57	Sequence 57, Appl	503	12.8	9.2	24	11	US-09-997-440-481	Sequence 481, App
C 431	13	9.4	26	11	US-09-872-712-3	Sequence 3, Appl	504	12.8	9.2	24	11	US-09-990-440-481	Sequence 481, App
C 432	13	9.4	26	14	US-10-010-476-76	Sequence 76, Appl	505	12.8	9.2	24	11	US-09-993-469-481	Sequence 481, App
C 433	13	9.4	27	10	US-09-758-269-19	Sequence 19, Appl	506	12.8	9.2	24	11	US-09-993-542-481	Sequence 481, App
C 434	13	9.4	27	11	US-09-961-077-1105	Sequence 1105, Ap	507	12.8	9.2	24	11	US-09-993-748-481	Sequence 481, App
C 435	13	9.4	28	10	US-09-887-576-426	Sequence 426, App	508	12.8	9.2	24	11	US-09-990-439-481	Sequence 481, App
C 436	13	9.4	28	14	US-10-169-580-11	Sequence 11, Appl	509	12.8	9.2	24	11	US-09-990-427-481	Sequence 481, App
C 437	13	9.4	29	9	US-09-745-763-57	Sequence 57, Appl	510	12.8	9.2	24	11	US-09-989-328-481	Sequence 481, App
C 438	13	9.4	29	12	US-10-300-341-40	Sequence 40, Appl	511	12.8	9.2	24	11	US-09-993-583-481	Sequence 481, App
C 439	13	9.4	29	14	US-10-079-384-38	Sequence 38, Appl	512	12.8	9.2	24	11	US-09-941-992-481	Sequence 481, App
C 440	13	9.4	30	9	US-09-771-425-3	Sequence 3, Appl	513	12.8	9.2	24	11	US-09-992-521-481	Sequence 481, App
C 441	13	9.4	30	9	US-09-874-138-9	Sequence 9, Appl	514	12.8	9.2	24	11	US-09-997-333-481	Sequence 481, App
C 442	13	9.4	30	13	US-10-005-842-9	Sequence 9, Appl	515	12.8	9.2	24	11	US-09-997-384-481	Sequence 481, App
C 443	13	9.4	30	14	US-10-085-906-100	Sequence 100, App	516	12.8	9.2	24	11	US-09-940-185-156	Sequence 156, App
C 444	12.8	9.2	17	11	US-09-877-478-994	Sequence 994, App	517	12.8	9.2	24	11	US-09-940-185-156	Sequence 156, App
C 445	12.8	9.2	17	11	US-09-877-478-1614	Sequence 1614, Ap	518	12.8	9.2	24	11	US-09-940-185-2470	Sequence 2470, Ap
C 446	12.8	9.2	17	11	US-09-848-754A-2544	Sequence 2544, Ap	519	12.8	9.2	24	11	US-09-940-185-3371	Sequence 3371, Ap
C 447	12.8	9.2	19	12	US-10-224-003-20	Sequence 20, Appl	520	12.8	9.2	24	11	US-09-982-860-192	Sequence 192, App
C 448	12.8	9.2	19	12	US-10-224-003-181	Sequence 181, App	521	12.8	9.2	24	11	US-09-988-041-481	Sequence 481, App
C 449	12.8	9.2	20	11	US-09-950-840-32	Sequence 32, Appl	522	12.8	9.2	24	11	US-09-997-585-481	Sequence 481, App
C 450	12.8	9.2	20	11	US-09-948-002-56	Sequence 56, Appl	523	12.8	9.2	24	11	US-09-997-614-481	Sequence 481, App
C 451	12.8	9.2	20	11	US-09-784-674-441	Sequence 441, App	524	12.8	9.2	24	12	US-09-989-862-481	Sequence 481, App
C 452	12.8	9.2	20	11	US-09-784-674-442	Sequence 442, App	525	12.8	9.2	24	12	US-09-989-862-481	Sequence 481, App
C 453	12.8	9.2	20	11	US-09-784-674-443	Sequence 443, App	526	12.8	9.2	24	12	US-09-989-862-481	Sequence 481, App
C 454	12.8	9.2	20	11	US-09-784-674-444	Sequence 444, App	527	12.8	9.2	24	12	US-09-989-862-481	Sequence 481, App

528	12.8	9.2	25	9	US-09-866-108-5773	Sequence 5773, App	C 601	12.8	9.2	27	10	US-09-817-014-168	Sequence 168, App
529	12.8	9.2	25	9	US-09-866-108-5774	Sequence 5774, App	C 602	12.8	9.2	28	14	US-10-225-630-31	Sequence 21, Appl
C 530	12.8	9.2	25	9	US-09-866-108-10947	Sequence 10947, App	C 603	12.8	9.2	29	10	US-09-972-016-1	Sequence 1, Appl
C 531	12.8	9.2	25	9	US-09-866-108-10948	Sequence 10948, App	C 604	12.8	9.2	30	9	US-09-766-399-42	Sequence 42, Appl
C 532	12.8	9.2	25	9	US-09-866-108-10949	Sequence 10949, App	C 605	12.8	9.2	30	9	US-09-908-130-5	Sequence 5, Appl
C 533	12.8	9.2	25	9	US-09-866-108-11169	Sequence 11169, App	C 606	12.8	9.2	30	9	US-09-908-130-16	Sequence 16, Appl
C 534	12.8	9.2	25	9	US-09-866-108-11170	Sequence 11170, App	C 607	12.8	9.2	30	9	US-09-908-131-5	Sequence 5, Appl
C 535	12.8	9.2	25	9	US-09-866-108-13691	Sequence 13691, App	C 608	12.8	9.2	30	9	US-09-908-131-16	Sequence 16, Appl
C 536	12.8	9.2	25	9	US-09-866-108-13692	Sequence 13692, App	C 609	12.8	9.2	30	9	US-09-761-963-46	Sequence 46, Appl
C 537	12.8	9.2	25	9	US-09-866-108-14097	Sequence 14097, App	C 610	12.8	9.2	30	10	US-09-778-516A-3	Sequence 3, Appl
C 538	12.8	9.2	25	11	US-09-754-853A-508	Sequence 508, App	C 611	12.8	9.2	30	10	US-09-907-795-5	Sequence 5, Appl
C 539	12.8	9.2	25	11	US-09-883-153-103	Sequence 103, App	C 612	12.8	9.2	30	10	US-09-907-795-16	Sequence 16, Appl
C 540	12.8	9.2	25	11	US-09-974-546-32	Sequence 32, Appl	C 613	12.8	9.2	30	10	US-09-758-017A-12	Sequence 12, Appl
C 541	12.8	9.2	25	11	US-09-951-502A-13	Sequence 13, Appl	C 614	12.8	9.2	30	10	US-09-963-875-31	Sequence 31, Appl
C 542	12.8	9.2	25	11	US-09-952-665-248	Sequence 248, App	C 615	12.8	9.2	30	10	US-10-136-871-29	Sequence 29, Appl
C 543	12.8	9.2	25	11	US-09-940-185-4137	Sequence 4137, App	C 616	12.8	9.2	30	14	US-10-108-714-16	Sequence 16, Appl
C 544	12.8	9.2	25	11	US-09-940-185-4647	Sequence 4647, App	C 617	12.8	9.2	30	14	US-10-124-884-5	Sequence 5, Appl
C 545	12.8	9.2	25	11	US-09-864-636A-1370	Sequence 1370, App	C 618	12.8	9.2	30	14	US-10-124-884-16	Sequence 16, Appl
C 546	12.8	9.2	25	11	US-09-864-636A-1370	Sequence 1370, App	C 619	12.8	9.2	30	14	US-10-151-336-15	Sequence 15, Appl
C 547	12.8	9.2	25	14	US-10-215-112-1810	Sequence 1810, App	C 620	12.8	9.2	30	14	US-10-120-687-31	Sequence 31, Appl
C 548	12.8	9.2	25	14	US-10-215-112-4287	Sequence 4287, App	C 621	12.8	9.2	30	14	US-10-202-428-6	Sequence 6, Appl
C 549	12.8	9.2	25	14	US-10-215-112-4797	Sequence 4797, App	C 622	12.8	9.2	30	14	US-10-283-300-46	Sequence 46, Appl
C 550	12.8	9.2	25	14	US-10-215-112-7458	Sequence 7458, App	C 623	12.8	9.2	30	14	US-08-983-605-55	Sequence 55, Appl
C 551	12.8	9.2	25	14	US-10-215-112-7584	Sequence 7584, App	C 624	12.8	9.2	30	7	US-08-731-499-40	Sequence 40, Appl
C 552	12.8	9.2	25	14	US-10-215-112-7899	Sequence 7899, App	C 625	12.8	9.2	20	8	US-08-983-605-448	Sequence 448, App
C 553	12.8	9.2	25	14	US-10-098-263B-6307	Sequence 6307, App	C 626	12.8	9.2	20	9	US-09-854-883-41	Sequence 41, Appl
C 554	12.8	9.2	25	14	US-10-098-263B-6567	Sequence 6567, App	C 627	12.8	9.2	20	11	US-09-773-307B-20	Sequence 20, Appl
C 555	12.8	9.2	25	14	US-10-098-263B-20045	Sequence 20045, App	C 628	12.8	9.2	20	11	US-09-931-375A-28	Sequence 28, Appl
C 556	12.8	9.2	25	14	US-10-098-263B-21720	Sequence 21720, App	C 629	12.8	9.2	20	11	US-09-802-640-51	Sequence 51, Appl
C 557	12.8	9.2	25	14	US-10-098-263B-22771	Sequence 22771, App	C 630	12.8	9.2	20	11	US-09-865-866-155	Sequence 155, App
C 558	12.8	9.2	25	14	US-10-098-263B-23963	Sequence 23963, App	C 631	12.8	9.2	20	11	US-09-784-674-586	Sequence 586, App
C 559	12.8	9.2	25	14	US-10-098-263B-29237	Sequence 29237, App	C 632	12.8	9.2	20	11	US-09-784-674-588	Sequence 588, App
C 560	12.8	9.2	25	14	US-10-098-263B-33293	Sequence 33293, App	C 633	12.8	9.2	20	11	US-09-952-522B-48	Sequence 48, Appl
C 561	12.8	9.2	25	14	US-10-098-263B-33294	Sequence 33294, App	C 634	12.8	9.2	20	12	US-10-020-478-66	Sequence 66, Appl
C 562	12.8	9.2	25	14	US-10-098-263B-33487	Sequence 33487, App	C 635	12.8	9.2	20	14	US-10-158-160A-50	Sequence 50, Appl
C 563	12.8	9.2	25	14	US-10-098-263B-34452	Sequence 34452, App	C 636	12.8	9.2	20	14	US-10-181-846-72	Sequence 72, Appl
C 564	12.8	9.2	25	14	US-10-098-263B-36816	Sequence 36816, App	C 637	12.8	9.2	20	14	US-10-213-452A-18	Sequence 18, Appl
C 565	12.8	9.2	25	14	US-10-098-263B-38061	Sequence 38061, App	C 638	12.8	9.2	21	9	US-09-765-081-398	Sequence 398, App
C 566	12.8	9.2	25	14	US-10-098-263B-41010	Sequence 41010, App	C 639	12.8	9.2	21	12	US-10-184-085A-399	Sequence 399, App
C 567	12.8	9.2	25	14	US-10-098-263B-41486	Sequence 41486, App	C 640	12.8	9.2	21	14	US-10-081-969-22	Sequence 22, Appl
C 568	12.8	9.2	25	14	US-10-098-263B-43881	Sequence 43881, App	C 641	12.8	9.2	21	14	US-10-081-969-67	Sequence 67, Appl
C 569	12.8	9.2	25	14	US-10-098-263B-59533	Sequence 59533, App	C 642	12.8	9.2	21	14	US-10-081-969-84	Sequence 84, Appl
C 570	12.8	9.2	25	14	US-10-098-263B-60161	Sequence 60161, App	C 643	12.8	9.2	21	22	US-09-305-856B-113	Sequence 113, App
C 571	12.8	9.2	25	14	US-10-098-263B-60672	Sequence 60672, App	C 644	12.8	9.2	22	9	US-09-966-880A-21	Sequence 21, Appl
C 572	12.8	9.2	25	14	US-10-098-263B-63082	Sequence 63082, App	C 645	12.8	9.2	23	10	US-10-266-463A-8	Sequence 8, Appl
C 573	12.8	9.2	25	14	US-10-098-263B-63583	Sequence 63583, App	C 646	12.8	9.2	23	12	US-10-105-200A-8	Sequence 8, Appl
C 574	12.8	9.2	25	14	US-10-098-263B-64259	Sequence 64259, App	C 647	12.8	9.2	23	14	US-10-105-504A-8	Sequence 8, Appl
C 575	12.8	9.2	25	14	US-10-098-263B-65413	Sequence 65413, App	C 648	12.8	9.2	23	14	US-10-105-504A-8	Sequence 8, Appl
C 576	12.8	9.2	25	14	US-10-098-263B-65507	Sequence 65507, App	C 649	12.8	9.2	23	14	US-10-105-504A-8	Sequence 8, Appl
C 577	12.8	9.2	25	14	US-10-098-263B-65508	Sequence 65508, App	C 650	12.8	9.2	24	7	US-08-731-499-37	Sequence 37, Appl
C 578	12.8	9.2	25	14	US-10-098-263B-66871	Sequence 66871, App	C 651	12.8	9.2	24	9	US-09-784-423-87	Sequence 87, Appl
C 579	12.8	9.2	25	14	US-10-098-263B-66872	Sequence 66872, App	C 652	12.8	9.2	24	11	US-09-940-185-1693	Sequence 1693, App
C 580	12.8	9.2	25	14	US-10-098-263B-68215	Sequence 68215, App	C 653	12.8	9.2	24	12	US-10-278-087A-15	Sequence 15, Appl
C 581	12.8	9.2	25	14	US-10-098-263B-68216	Sequence 68216, App	C 654	12.8	9.2	25	11	US-09-883-152-112	Sequence 112, App
C 582	12.8	9.2	25	14	US-10-098-263B-74887	Sequence 74887, App	C 655	12.8	9.2	25	14	US-10-215-112-5692	Sequence 5692, App
C 583	12.8	9.2	25	14	US-10-098-263B-74888	Sequence 74888, App	C 656	12.8	9.2	25	14	US-10-215-112-6455	Sequence 6455, App
C 584	12.8	9.2	25	14	US-10-098-263B-80275	Sequence 80275, App	C 657	12.8	9.2	25	14	US-10-215-112-6581	Sequence 6581, App
C 585	12.8	9.2	25	14	US-10-098-263B-80275	Sequence 80275, App	C 658	12.8	9.2	25	14	US-10-215-112-13966	Sequence 13966, App
C 586	12.8	9.2	25	14	US-10-098-263B-98808	Sequence 98808, App	C 659	12.8	9.2	25	14	US-10-098-263B-1109	Sequence 1109, App
C 587	12.8	9.2	25	14	US-10-098-263B-101857	Sequence 101857, App	C 660	12.8	9.2	25	14	US-10-098-263B-6901	Sequence 6901, App
C 588	12.8	9.2	25	14	US-10-098-263B-105050	Sequence 105050, App	C 661	12.8	9.2	25	14	US-10-098-263B-6902	Sequence 6902, App
C 589	12.8	9.2	25	14	US-10-098-263B-106423	Sequence 106423, App	C 662	12.8	9.2	25	14	US-10-098-263B-12633	Sequence 12633, App
C 590	12.8	9.2	25	14	US-10-098-263B-111257	Sequence 111257, App	C 663	12.8	9.2	25	14	US-10-098-263B-16234	Sequence 16234, App
C 591	12.8	9.2	25	14	US-10-098-263B-111893	Sequence 111893, App	C 664	12.8	9.2	25	14	US-10-098-263B-16234	Sequence 16234, App
C 592	12.8	9.2	25	14	US-10-098-263B-112159	Sequence 112159, App	C 665	12.8	9.2	25	14	US-10-098-263B-21266	Sequence 21266, App
C 593	12.8	9.2	25	14	US-10-098-263B-117967	Sequence 117967, App	C 666	12.8	9.2	25	14	US-10-098-263B-23985	Sequence 23985, App
C 594	12.8	9.2	25	14	US-10-098-263B-120713	Sequence 120713, App	C 667	12.8	9.2	25	14	US-10-098-263B-23986	Sequence 23986, App
C 595	12.8	9.2	25	14	US-10-098-263B-120904	Sequence 120904, App	C 668	12.8	9.2	25	14	US-10-098-263B-24333	Sequence 24333, App
C 596	12.8	9.2	25	14	US-10-098-263B-123926	Sequence 123926, App	C 669	12.8	9.2	25	14	US-10-098-263B-30204	Sequence 30204, App
C 597	12.8	9.2	25	14	US-10-098-263B-130699	Sequence 130699, App	C 670	12.8	9.2	25	14	US-10-098-263B-30812	Sequence 30812, App
C 598	12.8	9.2	25	14	US-10-098-263B-130709	Sequence 130709, App	C 671	12.8	9.2	25	14	US-10-098-263B-34523	Sequence 34523, App
C 599	12.8	9.2	26	11	US-09-991-262-38	Sequence 38, Appl	C 672	12.8	9.2	25	14	US-10-098-263B-34854	Sequence 34854, App
C 600	12.8	9.2	27	10	US-09-817-014-163	Sequence 163, Appl	C 673	12.8	9.2	25	14	US-10-098-263B-36720	Sequence 36720, App

C 674	12.6	9.1	25	14	US-10-098-263B-42319	Sequence 42319, A	C 747	12.6	9.1	30	15	US-10-219-935-7	Sequence 7, Appli
C 675	12.6	9.1	25	14	US-10-098-263B-42320	Sequence 42320, A	C 748	12.4	8.9	17	11	US-09-818-875-3470	Sequence 3470, Ap
C 676	12.6	9.1	25	14	US-10-098-263B-43047	Sequence 43047, A	C 749	12.4	8.9	17	11	US-09-818-875-3471	Sequence 3471, Ap
C 677	12.6	9.1	25	14	US-10-098-263B-47613	Sequence 47613, A	C 750	12.4	8.9	17	11	US-09-877-478-386	Sequence 386, App
C 678	12.6	9.1	25	14	US-10-098-263B-51824	Sequence 51824, A	C 751	12.4	8.9	17	11	US-09-877-478-386	Sequence 386, App
C 679	12.6	9.1	25	14	US-10-098-263B-53457	Sequence 53457, A	C 752	12.4	8.9	17	11	US-09-827-395A-479	Sequence 479, App
C 680	12.6	9.1	25	14	US-10-098-263B-53496	Sequence 53496, A	C 753	12.4	8.9	17	11	US-09-827-395A-479	Sequence 479, App
C 681	12.6	9.1	25	14	US-10-098-263B-56727	Sequence 56727, A	C 754	12.4	8.9	18	10	US-09-822-722-18	Sequence 18, Appl
C 682	12.6	9.1	25	14	US-10-098-263B-58013	Sequence 58013, A	C 755	12.4	8.9	18	10	US-09-822-722-18	Sequence 18, Appl
C 683	12.6	9.1	25	14	US-10-098-263B-60646	Sequence 60646, A	C 756	12.4	8.9	18	10	US-09-822-722-18	Sequence 18, Appl
C 684	12.6	9.1	25	14	US-10-098-263B-60644	Sequence 60644, A	C 757	12.4	8.9	19	11	US-09-728-552-1	Sequence 1, Appli
C 685	12.6	9.1	25	14	US-10-098-263B-67854	Sequence 67854, A	C 758	12.4	8.9	20	9	US-09-452-599-131	Sequence 131, App
C 686	12.6	9.1	25	14	US-10-098-263B-68517	Sequence 68517, A	C 759	12.4	8.9	20	10	US-09-987-025-8	Sequence 8, Appli
C 687	12.6	9.1	25	14	US-10-098-263B-77270	Sequence 77270, A	C 760	12.4	8.9	20	11	US-09-784-674-439	Sequence 439, App
C 688	12.6	9.1	25	14	US-10-098-263B-89624	Sequence 89624, A	C 761	12.4	8.9	20	11	US-09-784-674-446	Sequence 446, App
C 689	12.6	9.1	25	14	US-10-098-263B-90659	Sequence 90659, A	C 762	12.4	8.9	20	11	US-09-784-674-446	Sequence 446, App
C 690	12.6	9.1	25	14	US-10-098-263B-94422	Sequence 94422, A	C 763	12.4	8.9	20	11	US-09-906-158-107	Sequence 107, App
C 691	12.6	9.1	25	14	US-10-098-263B-102429	Sequence 102429, A	C 764	12.4	8.9	20	11	US-09-906-158-107	Sequence 107, App
C 692	12.6	9.1	25	14	US-10-098-263B-105219	Sequence 105219, A	C 765	12.4	8.9	20	13	US-09-917-963-93	Sequence 93, Appl
C 693	12.6	9.1	25	14	US-10-098-263B-105726	Sequence 105726, A	C 766	12.4	8.9	20	13	US-10-081-163-2	Sequence 2, Appli
C 694	12.6	9.1	25	14	US-10-098-263B-115270	Sequence 115270, A	C 767	12.4	8.9	21	14	US-10-149-352-5	Sequence 5, Appli
C 695	12.6	9.1	25	14	US-10-098-263B-118660	Sequence 118660, A	C 768	12.4	8.9	21	14	US-10-081-775-67	Sequence 67, Appli
C 696	12.6	9.1	25	14	US-10-098-263B-118904	Sequence 118904, A	C 769	12.4	8.9	22	9	US-09-834-795A-10	Sequence 10, Appl
C 697	12.6	9.1	25	14	US-10-098-263B-119249	Sequence 119249, A	C 770	12.4	8.9	22	9	US-09-834-795A-14	Sequence 14, Appl
C 698	12.6	9.1	25	14	US-10-098-263B-122343	Sequence 122343, A	C 771	12.4	8.9	22	11	US-09-834-794A-10	Sequence 10, Appl
C 699	12.6	9.1	25	14	US-10-098-263B-124966	Sequence 124966, A	C 772	12.4	8.9	22	11	US-09-834-794A-14	Sequence 14, Appl
C 700	12.6	9.1	26	11	US-09-439-429-13	Sequence 43, Appl</							

C 820	12.4	8.9	24	14	US-10-017-081A-93	Sequence 93, Appl	893	12.4	8.9	25	14	US-10-098-263B-43762	Sequence 43762, A
C 821	12.4	8.9	24	14	US-10-167-749-93	Sequence 93, Appl	C 894	12.4	8.9	25	14	US-10-098-263B-45883	Sequence 45883, A
C 822	12.4	8.9	24	14	US-10-095-672A-63	Sequence 63, Appl	C 895	12.4	8.9	25	14	US-10-098-263B-46375	Sequence 46375, A
C 823	12.4	8.9	24	14	US-10-095-672A-79	Sequence 79, Appl	C 896	12.4	8.9	25	14	US-10-098-263B-46993	Sequence 46993, A
C 824	12.4	8.9	24	14	US-10-013-921A-93	Sequence 93, Appl	C 897	12.4	8.9	25	14	US-10-098-263B-48583	Sequence 48583, A
C 825	12.4	8.9	24	14	US-10-013-929A-93	Sequence 93, Appl	C 898	12.4	8.9	25	14	US-10-098-263B-49447	Sequence 49447, A
C 826	12.4	8.9	24	14	US-10-016-177A-93	Sequence 93, Appl	C 899	12.4	8.9	25	14	US-10-098-263B-57769	Sequence 57769, A
C 827	12.4	8.9	24	14	US-10-166-709A-93	Sequence 93, Appl	900	12.4	8.9	25	14	US-10-098-263B-57769	Sequence 57769, A
C 828	12.4	8.9	25	9	US-09-866-108-4375	Sequence 4375, Ap	901	12.4	8.9	25	14	US-10-098-263B-61298	Sequence 61298, A
C 829	12.4	8.9	25	9	US-09-866-108-4376	Sequence 4376, Ap	902	12.4	8.9	25	14	US-10-098-263B-66287	Sequence 66287, A
C 830	12.4	8.9	25	9	US-09-866-108-4377	Sequence 4377, Ap	903	12.4	8.9	25	14	US-10-098-263B-66287	Sequence 66287, A
C 831	12.4	8.9	25	9	US-09-866-108-4378	Sequence 4378, Ap	C 904	12.4	8.9	25	14	US-10-098-263B-66795	Sequence 66795, A
C 832	12.4	8.9	25	9	US-09-866-108-4378	Sequence 4378, Ap	C 905	12.4	8.9	25	14	US-10-098-263B-66795	Sequence 66795, A
C 833	12.4	8.9	25	9	US-09-866-108-11280	Sequence 11280, A	C 906	12.4	8.9	25	14	US-10-098-263B-68475	Sequence 68475, A
C 834	12.4	8.9	25	9	US-09-866-108-11287	Sequence 11287, A	C 907	12.4	8.9	25	14	US-10-098-263B-68475	Sequence 68475, A
C 835	12.4	8.9	25	9	US-09-866-108-12968	Sequence 12968, A	C 908	12.4	8.9	25	14	US-10-098-263B-68899	Sequence 68899, A
C 836	12.4	8.9	25	9	US-09-866-108-12968	Sequence 12968, A	C 909	12.4	8.9	25	14	US-10-098-263B-69093	Sequence 69093, A
C 837	12.4	8.9	25	9	US-09-866-108-12970	Sequence 12970, A	C 910	12.4	8.9	25	14	US-10-098-263B-70346	Sequence 70346, A
C 838	12.4	8.9	25	9	US-09-866-108-12971	Sequence 12971, A	C 911	12.4	8.9	25	14	US-10-098-263B-71801	Sequence 71801, A
C 839	12.4	8.9	25	9	US-09-866-108-15099	Sequence 15099, A	C 912	12.4	8.9	25	14	US-10-098-263B-80749	Sequence 80749, A
C 840	12.4	8.9	25	9	US-09-866-108-15103	Sequence 15103, A	C 913	12.4	8.9	25	14	US-10-098-263B-82778	Sequence 82778, A
C 841	12.4	8.9	25	10	US-09-452-599-52	Sequence 52, Appl	C 914	12.4	8.9	25	14	US-10-098-263B-82778	Sequence 82778, A
C 842	12.4	8.9	25	10	US-09-528-175-33	Sequence 33, Appl	C 915	12.4	8.9	25	14	US-10-098-263B-83342	Sequence 83342, A
C 843	12.4	8.9	25	11	US-09-528-175-34	Sequence 34, Appl	C 916	12.4	8.9	25	14	US-10-098-263B-83342	Sequence 83342, A
C 844	12.4	8.9	25	11	US-09-754-853A-493	Sequence 493, Appl	C 917	12.4	8.9	25	14	US-10-098-263B-83938	Sequence 83938, A
C 845	12.4	8.9	25	11	US-09-754-853A-827	Sequence 827, Appl	C 918	12.4	8.9	25	14	US-10-098-263B-84858	Sequence 84858, A
C 846	12.4	8.9	25	11	US-09-883-152-107	Sequence 107, Appl	C 919	12.4	8.9	25	14	US-10-098-263B-84858	Sequence 84858, A
C 847	12.4	8.9	25	11	US-09-258-133-27	Sequence 27, Appl	C 920	12.4	8.9	25	14	US-10-098-263B-86931	Sequence 86931, A
C 848	12.4	8.9	25	11	US-09-269-921-41	Sequence 41, Appl	C 921	12.4	8.9	25	14	US-10-098-263B-86931	Sequence 86931, A
C 849	12.4	8.9	25	11	US-09-509-098-63	Sequence 63, Appl	C 922	12.4	8.9	25	14	US-10-098-263B-89938	Sequence 89938, A
C 850	12.4	8.9	25	14	US-10-076-597-29	Sequence 29, Appl	C 923	12.4	8.9	25	14	US-10-098-263B-89938	Sequence 89938, A
C 851	12.4	8.9	25	14	US-10-060-756A-2951	Sequence 2951, Ap	C 924	12.4	8.9	25	14	US-10-098-263B-95443	Sequence 95443, A
C 852	12.4	8.9	25	14	US-10-060-756A-2955	Sequence 2955, Ap	C 925	12.4	8.9	25	14	US-10-098-263B-95443	Sequence 95443, A
C 853	12.4	8.9	25	14	US-10-215-112-2673	Sequence 2673, Ap	C 926	12.4	8.9	25	14	US-10-098-263B-95533	Sequence 95533, A
C 854	12.4	8.9	25	14	US-10-215-112-6072	Sequence 6072, Ap	C 927	12.4	8.9	25	14	US-10-098-263B-95533	Sequence 95533, A
C 855	12.4	8.9	25	14	US-10-215-112-6307	Sequence 6307, Ap	C 928	12.4	8.9	25	14	US-10-098-263B-95853	Sequence 95853, A
C 856	12.4	8.9	25	14	US-10-215-112-6433	Sequence 6433, Ap	C 929	12.4	8.9	25	14	US-10-098-263B-98255	Sequence 98255, A
C 857	12.4	8.9	25	14	US-10-215-112-6569	Sequence 6569, Ap	C 930	12.4	8.9	25	14	US-10-098-263B-98255	Sequence 98255, A
C 858	12.4	8.9	25	14	US-10-215-112-8530	Sequence 8530, Ap	C 931	12.4	8.9	25	14	US-10-098-263B-98907	Sequence 98907, A
C 859	12.4	8.9	25	14	US-10-215-112-10856	Sequence 10856, Ap	C 932	12.4	8.9	25	14	US-10-098-263B-99677	Sequence 99677, A
C 860	12.4	8.9	25	14	US-10-215-112-11490	Sequence 11490, A	C 933	12.4	8.9	25	14	US-10-098-263B-100258	Sequence 100258, A
C 861	12.4	8.9	25	14	US-10-215-112-11503	Sequence 11503, A	C 934	12.4	8.9	25	14	US-10-098-263B-102451	Sequence 102451, A
C 862	12.4	8.9	25	14	US-10-215-112-11629	Sequence 11629, A	C 935	12.4	8.9	25	14	US-10-098-263B-102451	Sequence 102451, A
C 863	12.4	8.9	25	14	US-10-215-112-11823	Sequence 11823, A	C 936	12.4	8.9	25	14	US-10-098-263B-105767	Sequence 105767, A
C 864	12.4	8.9	25	14	US-10-215-112-13406	Sequence 13406, A	C 937	12.4	8.9	25	14	US-10-098-263B-105767	Sequence 105767, A
C 865	12.4	8.9	25	14	US-10-215-112-14317	Sequence 14317, A	C 938	12.4	8.9	25	14	US-10-098-263B-106305	Sequence 106305, A
C 866	12.4	8.9	25	14	US-10-215-112-14443	Sequence 14443, A	C 939	12.4	8.9	25	14	US-10-098-263B-106305	Sequence 106305, A
C 867	12.4	8.9	25	14	US-10-098-263B-3832	Sequence 3832, Ap	C 940	12.4	8.9	25	14	US-10-098-263B-106468	Sequence 106468, A
C 868	12.4	8.9	25	14	US-10-098-263B-3979	Sequence 3979, Ap	C 941	12.4	8.9	25	14	US-10-098-263B-106468	Sequence 106468, A
C 869	12.4	8.9	25	14	US-10-098-263B-5771	Sequence 5771, Ap	C 942	12.4	8.9	25	14	US-10-098-263B-112389	Sequence 112389, A
C 870	12.4	8.9	25	14	US-10-098-263B-8611	Sequence 8611, Ap	C 943	12.4	8.9	25	14	US-10-098-263B-112389	Sequence 112389, A
C 871	12.4	8.9	25	14	US-10-098-263B-14443	Sequence 14443, A	C 944	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 872	12.4	8.9	25	14	US-10-098-263B-16462	Sequence 16462, A	C 945	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 873	12.4	8.9	25	14	US-10-098-263B-16827	Sequence 16827, A	C 946	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 874	12.4	8.9	25	14	US-10-098-263B-19886	Sequence 19886, A	C 947	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 875	12.4	8.9	25	14	US-10-098-263B-22965	Sequence 22965, A	C 948	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 876	12.4	8.9	25	14	US-10-098-263B-25173	Sequence 25173, A	C 949	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 877	12.4	8.9	25	14	US-10-098-263B-27276	Sequence 27276, A	C 950	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 878	12.4	8.9	25	14	US-10-098-263B-28941	Sequence 28941, A	C 951	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 879	12.4	8.9	25	14	US-10-098-263B-30681	Sequence 30681, A	C 952	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 880	12.4	8.9	25	14	US-10-098-263B-31688	Sequence 31688, A	C 953	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 881	12.4	8.9	25	14	US-10-098-263B-32305	Sequence 32305, A	C 954	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 882	12.4	8.9	25	14	US-10-098-263B-34350	Sequence 34350, A	C 955	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 883	12.4	8.9	25	14	US-10-098-263B-34797	Sequence 34797, A	C 956	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 884	12.4	8.9	25	14	US-10-098-263B-34988	Sequence 34988, A	C 957	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 885	12.4	8.9	25	14	US-10-098-263B-37684	Sequence 37684, A	C 958	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 886	12.4	8.9	25	14	US-10-098-263B-37693	Sequence 37693, A	C 959	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 887	12.4	8.9	25	14	US-10-098-263B-38244	Sequence 38244, A	C 960	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 888	12.4	8.9	25	14	US-10-098-263B-40196	Sequence 40196, A	C 961	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 889	12.4	8.9	25	14	US-10-098-263B-40745	Sequence 40745, A	C 962	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 890	12.4	8.9	25	14	US-10-098-263B-40865	Sequence 40865, A	C 963	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 891	12.4	8.9	25	14	US-10-098-263B-41776	Sequence 41776, A	C 964	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
C 892	12.4	8.9	25	14	US-10-098-263B-41966	Sequence 41966, A	C 965	12.4	8.9	25	14	US-10-098-263B-112492	Sequence 112492, A
					Sequence 43055, A	Sequence 43055, A							

; FILE REFERENCE: ISPH-0596
; CURRENT APPLICATION NUMBER: US/09/925,139
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-29

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CTGGAACCTGGTGTCTCCT 60
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CTGGAACCTGGTGTCTCCT 1

RESULT 5

US-09-925-139-30/c
; Sequence 30, Application US/09925139
; Publication No. US20030092647A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Pam Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRE
; FILE REFERENCE: ISPH-0596
; CURRENT APPLICATION NUMBER: US/09/925,139
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-30

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 GGAAGTTGGTTAGGAGTAC 90
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GGAAGTTGGTTAGGAGTAC 1

RESULT 6

US-09-925-139-47/c
; Sequence 47, Application US/09925139
; Publication No. US20030092647A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Pam Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRE
; FILE REFERENCE: ISPH-0596
; CURRENT APPLICATION NUMBER: US/09/925,139
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-49

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 GGAGTACGAGATGGAGATT 103

; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-47

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GCTTGTAGCAGAGGCAAGC 27
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GCTTGTAGCAGAGGCAAGC 1

RESULT 7

US-09-925-139-48/c
; Sequence 48, Application US/09925139
; Publication No. US20030092647A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Pam Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRE
; FILE REFERENCE: ISPH-0596
; CURRENT APPLICATION NUMBER: US/09/925,139
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-48

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGCGTGGTGGAGTTGGGTT 82
| | | | | | | | | | | | | | | | | | | | | |
Db 20 AGCGTGGTGGAGTTGGGTT 1

RESULT 8

US-09-925-139-49/c
; Sequence 49, Application US/09925139
; Publication No. US20030092647A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Pam Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRE
; FILE REFERENCE: ISPH-0596
; CURRENT APPLICATION NUMBER: US/09/925,139
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-49

Query Match 14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 GGAGTACGAGATGGAGATT 103

```
Db      20  GGAGTACGGAGATGGAGATT 1
|||||
RESULT 9
US-09-925-139-50/c
; Sequence 50, Application US/09925139
; Publication No. US20030092647A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; APPLICANT: Pam Nero
; APPLICANT: Edward Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN EXPRES
; FILE REFERENCE: ISPH-0596
; CURRENT APPLICATION NUMBER: US/09/925.139
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-925-139-50

Query Match      14.4%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Qy      120  CTATCCTAAAGGCCCACTGG 139
|||||
Db      20  CTATCCTAAAGGCCCACTGG 1

RESULT 10
US-09-941-094A-1
; Sequence 1, Application US/09941094A
; Patent No. US20020065226A1
; GENERAL INFORMATION:
; APPLICANT: Siler-Khodr, Theresa M.
; TITLE OF INVENTION: No. US20020065226A1-Mammalian GnRH Analogs and Uses Thereof in Re
; TITLE OF INVENTION: Pregnancy
; FILE REFERENCE: P7345.2(CIP)
; CURRENT APPLICATION NUMBER: US/09/941,094A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 09/419,161
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Gallus gallus
US-09-941-094A-1

Query Match      12.1%; Score 16.8; DB 9; Length 30;
Best Local Similarity 75.0%; Pred. No. 2.9e+04;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      25  AGCACCAGGCTCAGCTGGAACCTGG 52
|||||
Db      2  AGCACTGGTCCCATGGCTGTACCTGG 29

RESULT 11
US-09-865-866-13/c
; Sequence 13, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
```

```
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865.866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 13
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-09-865-866-13
```

```
Query Match      11.8%; Score 16.4; DB 11; Length 30;
Best Local Similarity 76.9%; Pred. No. 3.9e+04;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      87  GTACGGAGATGGAGATGGCTCCCAA 112
|||||
Db      28  GTACGAGAGAGAGAGTGGATGCCAA 3
```

```
RESULT 12
US-10-098-263B-25768
; Sequence 25768, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 25768
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-25768
```

```
Query Match      11.1%; Score 15.4; DB 14; Length 25;
Best Local Similarity 94.1%; Pred. No. 8.5e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      86  AGTACGGAGATGGAGAT 102
|||||
Db      2  AGTACTGAGATGGAGAT 18
```

```
RESULT 13
US-10-098-263B-15079
; Sequence 15079, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 15079
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-15079
```

```
Query Match      10.9%; Score 15.2; DB 14; Length 25;
Best Local Similarity 85.0%; Pred. No. 1e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 43 GGAACCCCTGGTGTCTCTCC 62
Db 5 GGAACCCCTGGTGTCTCAGTCC 24

RESULT 14

US-09-908-130-18
; Sequence 18, Application US/09908130
; Patent No. US20020051992A1
; GENERAL INFORMATION:
; APPLICANT: Bridgham, John
; APPLICANT: Corcoran, Kevin P.
; APPLICANT: Golda, George S.
; APPLICANT: Brenner, Sydney
; APPLICANT: Pallas, Michael C.
; TITLE OF INVENTION: System and Apparatus for Sequential
; TITLE OF INVENTION: Processing of Analytes
; FILE REFERENCE: 5525-0035.22
; CURRENT APPLICATION NUMBER: US/09/908,130
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 09/424,028
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: PCT/US98/11224
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 08/862,610
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic encoded adaptor
; NAME/KEY: misc feature
; LOCATION: (1)...(4)
; OTHER INFORMATION: n = A,T,C or G
US-09-908-130-18

Query Match 10.9%; Score 15.2; DB 9; Length 30;
Best Local Similarity 85.0%; Pred. No. 1e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 37 ACAGCTGGACCCCTGGTGTCTC 56
Db 6 ACAGCTGCATCCCTGGTGAC 25

RESULT 15

US-09-908-131-18
; Sequence 18, Application US/09908131
; Patent No. US20020061529A1
; GENERAL INFORMATION:
; APPLICANT: Bridgham, John
; APPLICANT: Corcoran, Kevin P.
; APPLICANT: Golda, George S.
; APPLICANT: Brenner, Sydney
; APPLICANT: Pallas, Michael C.
; TITLE OF INVENTION: System and Apparatus for Sequential
; TITLE OF INVENTION: Processing of Analytes
; FILE REFERENCE: 5525-0035.21
; CURRENT APPLICATION NUMBER: US/09/908,131
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 09/424,028
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: PCT/US98/11224
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 08/862,610
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18

; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic encoded adaptor
; NAME/KEY: misc feature
; LOCATION: (1)...(4)
; OTHER INFORMATION: n = A,T,C or G
US-09-908-131-18

Query Match 10.9%; Score 15.2; DB 9; Length 30;
Best Local Similarity 85.0%; Pred. No. 1e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 37 ACAGCTGGACCCCTGGTGTCTC 56
Db 6 ACAGCTGCATCCCTGGTGAC 25

RESULT 16

US-09-907-795-18
; Sequence 18, Application US/09907795
; Patent No. US20020137052A1
; GENERAL INFORMATION:
; APPLICANT: Bridgham, John
; APPLICANT: Corcoran, Kevin P.
; APPLICANT: Golda, George S.
; APPLICANT: Brenner, Sydney
; APPLICANT: Pallas, Michael C.
; TITLE OF INVENTION: System and Apparatus for Sequential
; TITLE OF INVENTION: Processing of Analytes
; FILE REFERENCE: 5525-0035.23
; CURRENT APPLICATION NUMBER: US/09/907,795
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 09/424,028
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: PCT/US98/11224
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 08/862,610
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic encoded adaptor
; NAME/KEY: misc feature
; LOCATION: (1)...(4)
; OTHER INFORMATION: n = A,T,C or G
US-09-907-795-18

Query Match 10.9%; Score 15.2; DB 10; Length 30;
Best Local Similarity 85.0%; Pred. No. 1e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 37 ACAGCTGGACCCCTGGTGTCTC 56
Db 6 ACAGCTGCATCCCTGGTGAC 25

RESULT 17

US-10-124-884-18
; Sequence 18, Application US/10124884
; Publication No. US2003007615A1
; GENERAL INFORMATION:
; APPLICANT: Bridgham, John
; APPLICANT: Corcoran, Kevin P.
; APPLICANT: Golda, George S.
; APPLICANT: Pallas, Michael C.
; APPLICANT: Brenner, Sydney
; TITLE OF INVENTION: Planar Arrays of Microparticle-Bound

```
; TITLE OF INVENTION: Polynucleotides
; FILE REFERENCE: 55525-8035:US05
; CURRENT APPLICATION NUMBER: US/10/124,884
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/424,028
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: PCT/US98/11224
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 08/862,610
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic encoded adaptor
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4)
; OTHER INFORMATION: n = A,T,C or G
US-10-124-884-18

Query Match      10.9%; Score 15.2; DB 14; Length 30;
Best Local Similarity 85.0%; Pred. No. 1e+05; 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 37 ACAGCTGGAACCTCGTGTC 56
      ||||| ||||| |||||
DB 6 ACAGCTGCATCCCTGGTGAC 25

RESULT 18
US-10-098-263B-4644/c
; Sequence 4644, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 4644
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-4644

Query Match      10.8%; Score 15; DB 14; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+05; 5; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 73 AAGTTGGGTTAGGAGTACGAGA 95
      ||||| ||||| ||||| |||||
DB 24 AAGTTCGGTGAGGAGTCCGTAGA 2

RESULT 19
US-10-098-263B-108698
; Sequence 108698, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759

; TITLE OF INVENTION: Polynucleotides
; FILE REFERENCE: 55525-8035:US05
; CURRENT APPLICATION NUMBER: US/10/124,884
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/424,028
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: PCT/US98/11224
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: US 08/862,610
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic encoded adaptor
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4)
; OTHER INFORMATION: n = A,T,C or G
US-10-124-884-18

Query Match      10.8%; Score 15; DB 14; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+05; 5; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 103 TGGCTCCCAACTCCTCCCTATCC 125
      ||||| ||||| ||||| |||||
DB 3 TAGGTCCCTACTCCGCTCTATCC 25

RESULT 20
US-10-098-263B-111973
; Sequence 111973, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111973
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-111973

Query Match      10.8%; Score 15; DB 14; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.2e+05; 5; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 114 TCCTCCCTATCCTAAAGCCAC 136
      ||||| ||||| ||||| |||||
DB 1 TTCTCCATATCTTAATGCCCC 23

RESULT 21
US-10-098-263B-121355/c
; Sequence 121355, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 121355
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-121355

Query Match      10.8%; Score 15; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+05; 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 TCCTCCAGCGTGGTG 71
      ||||| ||||| ||||| |||||
```

Db 25 TCCTCCAGCTGGTG 11

RESULT 22

US-09-923-246-31/c
; Sequence 31, Application US/09923246
; Patent No. US20020128446A1

GENERAL INFORMATION:

; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.

; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

; FILE REFERENCE: 99-16

; CURRENT APPLICATION NUMBER: US/09/923,246

; CURRENT FILING DATE: 2001-08-03

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 31

; LENGTH: 29

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide primer ZC19932

US-09-923-246-31

Query Match 10.8%; Score 15; DB 10; Length 29;
Best Local Similarity 78.3%; Pred. No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 40 GCTGGAACCTGGTGCTCTCTCC 62

Db 24 GCTGGAACCTCACGGATCTCTCC 2

RESULT 23

US-09-823-561A-22/c

; Sequence 22, Application US/09825561A

; Patent No. US20020137677A1

GENERAL INFORMATION:

; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.

; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS

; FILE REFERENCE: 00-22

; CURRENT APPLICATION NUMBER: US/09/825,561A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/194,731

; PRIOR FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/222,121

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 22

; LENGTH: 29

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide primer ZC19932

US-09-825-561A-22

Query Match 10.8%; Score 15; DB 10; Length 29;

Best Local Similarity 78.3%; Pred. No. 1.2e+05;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 40 GCTGGAACCTGGTGCTCTCTCTCC 62

Db 24 GCTGGAACCTCACGGATCTCTCC 2

RESULT 24

US-10-243-072-43/c

; Sequence 43, Application US/10243072

; Publication No. US20030148447A1

GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030148447A1ak, Julia E.
; APPLICANT: Hammond, Angela K.

; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHA11

; FILE REFERENCE: 98-55C1

; CURRENT APPLICATION NUMBER: US/10/243,072

; CURRENT FILING DATE: 2002-09-13

; PRIOR APPLICATION NUMBER: 09/628,127

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/100,896

; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: US 60/123,546

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: US 60/142,574

; PRIOR FILING DATE: 1999-07-06

; PRIOR APPLICATION NUMBER: US 09/404,641

; PRIOR FILING DATE: 1999-09-23

; NUMBER OF SEQ ID NOS: 92

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 43

; LENGTH: 29

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide primer ZC19932

US-10-243-072-43

Query Match 10.8%; Score 15; DB 12; Length 29;

Best Local Similarity 78.3%; Pred. No. 1.2e+05;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 40 GCTGGAACCTGGTGCTCTCTCTCC 62

Db 24 GCTGGAACCTCACGGATCTCTCC 2

RESULT 25

US-10-295-723-31/c

; Sequence 31, Application US/10295723

; Publication No. US20030125524A1

GENERAL INFORMATION:

; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.

; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

; FILE REFERENCE: 99-16

; CURRENT APPLICATION NUMBER: US/10/295,723

; CURRENT FILING DATE: 2002-11-15


```

; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC19932
US-10-295-723-31

Query Match      10.8%; Score 15; DB 14; Length 29;
Best Local Similarity 78.3%; Pred.No. 1.2e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      40 GCTGGAACCCCTGGTCTCTCTCC 62
        |||||
Db      24 GCTGGAACCCCTCAGGATCTCC 2

Search completed: August 22, 2003, 11:06:14
Job time : 168 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 09:57:54 ; Search time 1611 Seconds

(without alignments)

2097.034 Million cell updates/sec

Title: US-09-925-139-3_COPY_1631_1769

Perfect score: 139

Sequence: 1 ggaatgggggttagcagaa.....ctatcctaagggccactgg 139

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 33330

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.2	12.4	28	AZ609431	AZ609431 IM0434PI7
C 2	15	10.8	27	AZ330939	AZ330939 IM0056E11
C 3	14.6	10.5	24	AZ861819	AZ861819 2M0168L12
C 4	14.6	10.5	25	AZ453525	AZ453525 IM0255A01

C 78	12.2	8.8	29	8.8	AZ795012	2M0049104	151	11.6	8.3	28	28	AZ438215	1M0228K12
C 79	12.2	8.8	30	10	BE384733	601277335	152	11.6	8.3	28	28	AZ463404	1M0272011
C 80	12.2	8.8	30	28	AZ584820	1M0389A14	153	11.6	8.3	28	28	AZ784264	2M0026I20
C 81	12	8.6	22	9	AI444134	FB4401.Y	154	11.6	8.3	28	28	AZ792783	2M0045C01
C 82	12	8.6	22	29	TA376G03Q		155	11.6	8.3	28	28	BH810422	SALK_0495
C 83	12	8.6	23	28	AZ455732	2M0258B16	156	11.6	8.3	29	28	AZ346074	1M0081I05
C 84	12	8.6	25	29	AG253732	1M0258B16	157	11.6	8.3	29	28	AZ503753	1M0343H09
C 85	12	8.6	26	29	TA127E06P		158	11.6	8.3	29	28	AZ666737	1M0549006
C 86	12	8.6	27	9	AU255344	AU255344	159	11.6	8.3	29	28	BZ379180	SALK_1129
C 87	12	8.6	27	28	AZ465524	1M0333D04	160	11.6	8.3	30	10	BE274322	601121015
C 88	12	8.6	27	28	AZ783077	2M0024A01	161	11.6	8.3	30	10	BE274322	601121015
C 89	12	8.6	27	28	AZ817236	2M0086D03	162	11.6	8.3	30	28	BE280898	601155490
C 90	12	8.6	27	28	AZ836891	2M0131N22	163	11.6	8.3	30	28	AZ474193	1M0290J02
C 91	12	8.6	27	28	AZ840204	2M0136H08	164	11.6	8.3	30	28	BH866519	SALK_1014
C 92	12	8.6	28	9	AI919484	VZ20F02.F	165	11.4	8.2	17	12	AJ303573	Plasmodiu
C 93	12	8.6	28	28	AZ317107	1M0035E09	166	11.4	8.2	20	28	EM339359	50072-2-8
C 94	12	8.6	28	28	AZ737089	1M0584J23	167	11.4	8.2	21	28	EM339359	50072-2-8
C 95	12	8.6	29	9	AU258028	AU258028	168	11.4	8.2	22	9	AZ443821	1M0103A01
C 96	12	8.6	29	14	N27011	YW73B09.S1	169	11.4	8.2	22	9	AI677768	1M0238I07
C 97	12	8.6	29	29	CC179015	SALK_0570	170	11.4	8.2	22	9	AI748552	6B54F11.Y
C 98	12	8.6	29	28	BH418365	eco-Fl_Mu	171	11.4	8.2	22	9	AI748552	6B54F11.Y
C 99	12	8.6	30	28	BH418365	eco-Fl_Mu	172	11.4	8.2	22	9	AI748552	6B54F11.Y
C 100	11.8	8.5	22	28	AZ666649	1M0548M19	173	11.4	8.2	22	28	AZ608971	1M0433D04
C 101	11.8	8.5	24	28	AZ587901	1M0395F24	174	11.4	8.2	23	28	AZ305600	1M0006A19
C 102	11.8	8.5	24	28	AZ789936	2M0038L17	175	11.4	8.2	23	28	BH857265	SALK_0765
C 103	11.8	8.5	24	28	AZ812697	2M0079K05	176	11.4	8.2	23	29	TA130F01Q	
C 104	11.8	8.5	25	28	TA84A06P		177	11.4	8.2	24	28	AZ601725	1M0420E12
C 105	11.8	8.5	26	28	AZ782918	1M0024L10	178	11.4	8.2	24	28	AZ663558	1M0543E13
C 106	11.8	8.5	27	14	H84968	Y89C08.R1	179	11.4	8.2	24	28	AZ800048	2M0057C24
C 107	11.8	8.5	27	28	AZ416143	1M0191G14	180	11.4	8.2	25	9	AZ831249	2M0110G21
C 108	11.8	8.5	27	28	AZ623078	1M0460G19	181	11.4	8.2	25	9	AI000890	0856H04.S
C 109	11.8	8.5	27	28	AZ970595	2M0243I18	182	11.4	8.2	25	9	AI586975	tw15Q05.X
C 110	11.8	8.5	28	14	CO0171	HUMGS000582	183	11.4	8.2	25	28	AZ303792	1M0003H07
C 111	11.8	8.5	28	28	AZ623636	1M0461N05	184	11.4	8.2	25	28	AZ565950	1M0532M15
C 112	11.8	8.5	28	28	AZ776516	2M0010K24	185	11.4	8.2	25	28	BH789422	SALK_0293
C 113	11.8	8.5	28	28	AZ776516	2M0010K24	186	11.4	8.2	25	28	AZ842018	1M0306I16
C 114	11.8	8.5	29	28	AZ797506	2M0095M11	187	11.4	8.2	27	28	AZ586887	1M0394H09
C 115	11.8	8.5	29	28	AZ822427	2M0095M11	188	11.4	8.2	27	28	AI119990	uc25C01.F
C 116	11.8	8.5	30	10	B9207686	601178428	189	11.4	8.2	28	9	AI156146	ue08F05.F
C 117	11.8	8.5	30	10	B9200191	601673121	190	11.4	8.2	28	9	AI537875	tp32F04.X
C 118	11.8	8.5	30	28	AZ773368	1M0584A23	191	11.4	8.2	28	9	AI930845	8B43001.Y
C 119	11.8	8.5	30	29	AG230072		192	11.4	8.2	28	29	AZ500025	Drosophila
C 120	11.8	8.5	30	29	DR19J3S		193	11.4	8.2	28	29	AZ546620	Drosophila
C 121	11.6	8.3	19	28	AZ777470	1M0011H21	194	11.4	8.2	28	29	TA196808Q	
C 122	11.6	8.3	20	28	AZ308311	1M0011J12	195	11.4	8.2	28	29	AZ419519	1M0196N03
C 123	11.6	8.3	20	28	AZ331568	1M0059N03	196	11.4	8.2	28	29	AZ651322	1M0521P20
C 124	11.6	8.3	21	28	AZ978432	2M0254G15	197	11.4	8.2	28	29	AZ94050	2M0047H09
C 125	11.6	8.3	22	12	B925518	HNC5-1-C1	198	11.4	8.2	29	28	AZ817122	2M0086C16
C 126	11.6	8.3	22	12	B925518	HNC23-1-E	199	11.4	8.2	29	29	BZ377903	SALK_1063
C 127	11.6	8.3	22	13	BQ584930	E011828-0	200	11.4	8.2	29	29	TA211B01P	
C 128	11.6	8.3	22	28	AZ966411	2M0236E22	201	11.4	8.2	30	9	AU259645	AU259645
C 129	11.6	8.3	22	28	AZ966411	2M0236E22	202	11.4	8.2	30	10	BE883323	601509063
C 130	11.6	8.3	23	28	AZ400856	1M0167N17	203	11.4	8.2	30	12	BM393328	50071-2-9
C 131	11.6	8.3	23	28	AZ971749	2M0245C21	204	11.4	8.2	30	12	BM395411	50072-2-9
C 132	11.6	8.3	25	9	AA912548	Q136C01.S	205	11.4	8.2	30	12	BM395411	50072-2-9
C 133	11.6	8.3	25	28	AZ460726	1M0266010	206	11.4	8.2	30	12	BM395411	50072-2-9
C 134	11.6	8.3	26	12	BM888078	TMT492.Hu	207	11.4	8.2	30	12	BM395411	50072-2-9
C 135	11.6	8.3	26	28	AZ352012	1M0090M13	208	11.4	8.2	30	12	BM395411	50072-2-9
C 136	11.6	8.3	26	28	AZ462630	1M0269F08	209	11.4	8.2	30	12	BM395411	50072-2-9
C 137	11.6	8.3	26	28	BH907918	SALK_0448	210	11.4	8.2	30	12	BM395411	50072-2-9
C 138	11.6	8.3	27	9	AU259022		211	11.2	8.1	20	28	AZ320153	1M0376C18
C 139	11.6	8.3	27	28	AZ352726	1M0091N13	212	11.2	8.1	20	28	AZ320153	1M0376C18
C 140	11.6	8.3	27	28	AZ447932	2M0245013	213	11.2	8.1	20	28	AZ320153	1M0376C18
C 141	11.6	8.3	27	28	AZ835139	2M0129F09	214	11.2	8.1	20	28	AZ320153	1M0376C18
C 142	11.6	8.3	27	28	AZ981096	2M0258I20	215	11.2	8.1	20	28	AZ320153	1M0376C18
C 143	11.6	8.3	27	28	AZ999191	2M0286021	216	11.2	8.1	20	28	AZ320153	1M0376C18
C 144	11.6	8.3	28	9	AA761725	nz28g11.S	217	11.2	8.1	20	28	AZ320153	1M0376C18
C 145	11.6	8.3	28	9	AI023489	ov70H01.S	218	11.2	8.1	20	28	AZ320153	1M0376C18
C 146	11.6	8.3	28	9	AI023489	ov70H01.S	219	11.2	8.1	20	28	AZ320153	1M0376C18
C 147	11.6	8.3	28	14	N79189	zallid10.r1	220	11.2	8.1	20	28	AZ320153	1M0376C18
C 148	11.6	8.3	28	28	AZ312882	1M0029D05	221	11.2	8.1	20	28	AZ320153	1M0376C18
C 149	11.6	8.3	28	28	AZ345524	1M0080M01	222	11.2	8.1	20	28	AZ320153	1M0376C18
C 150	11.6	8.3	28	28	AZ346701	1M0082K06	223	11.2	8.1	20	28	AZ320153	1M0376C18

224	11.2	8.1	25	28	AZ937578	2M0195L17	AZ937578	2M0195L17	11	7.9	26	28	AZ357556	1M0099K10
225	11.2	8.1	25	29	TA237D08Q	AL481334 T. brucei	AL481334	T. brucei	11	7.9	26	28	AZ445168	1M0240J13
226	11.2	8.1	26	12	BG900896	BG900896 HOA7-1-A4	BG900896	HOA7-1-A4	11	7.9	26	28	AZ664004	1M0543019
227	11.2	8.1	26	28	AZ424207	1M0203N07	AZ424207	1M0203N07	11	7.9	26	28	AZ942099	2M0202C09
228	11.2	8.1	26	28	AZ499519	1M0337P15	AZ499519	1M0337P15	11	7.9	26	29	TA151E04P	AL467331 T. brucei
229	11.2	8.1	26	28	AZ632192	1M0486O12	AZ632192	1M0486O12	11	7.9	27	12	BM400457	5M09-0-73
230	11.2	8.1	27	14	D18734	MUSGS01796	D18734	MUSGS01796	11	7.9	27	28	AZ345323	1M0079M16
231	11.2	8.1	27	28	AZ479687	1M0300H02	AZ479687	1M0300H02	11	7.9	27	28	AZ465567	1M0275C17
232	11.2	8.1	27	28	AZ4793050	2M0024J21	AZ4793050	2M0024J21	11	7.9	27	28	AZ468814	1M0282G02
233	11.2	8.1	27	28	AZ873243	2M0103N04	AZ873243	2M0103N04	11	7.9	27	28	AZ473031	1M0288I12
234	11.2	8.1	27	28	AZ869647	2M0147P15	AZ869647	2M0147P15	11	7.9	27	28	AZ792850	2M0045B10
235	11.2	8.1	27	28	BH851753	SALK_0734	BH851753	SALK_0734	11	7.9	27	28	AZ919484	VZ2202F02.r
236	11.2	8.1	28	9	A1544609	fb76e03.x	A1544609	fb76e03.x	11	7.9	28	9	AZ994610	0c44d04.r
237	11.2	8.1	28	28	AZ363489	1M0109I06	AZ363489	1M0109I06	11	7.9	28	9	AA074506	zif82h09.r
238	11.2	8.1	28	28	AZ403083	1M0170P09	AZ403083	1M0170P09	11	7.9	28	9	A1769335	wg3601.x
239	11.2	8.1	28	28	AZ650845	1M0521B13	AZ650845	1M0521B13	11	7.9	28	28	AZ312487	1M0028B22
240	11.2	8.1	28	28	AZ790279	2M0338P08	AZ790279	2M0338P08	11	7.9	28	28	AZ312778	1M0028N11
241	11.2	8.1	28	28	AZ941528	2M0201L14	AZ941528	2M0201L14	11	7.9	28	28	AZ342196	1M0075F07
242	11.2	8.1	28	28	BH855787	SALK_0845	BH855787	SALK_0845	11	7.9	28	28	AZ502451	1M0341D17
243	11.2	8.1	28	29	BZ594385	SALK_0840	BZ594385	SALK_0840	11	7.9	28	28	AZ514612	1M0361M21
244	11.2	8.1	29	9	AU258464	AU258464	AU258464		11	7.9	28	28	AZ583963	1M0388J09
245	11.2	8.1	29	28	AZ424753	1M0204F04	AZ424753	1M0204F04	11	7.9	29	14	N85094	N85094 J2291F Huma
246	11.2	8.1	29	28	AZ840358	2M0136D22	AZ840358	2M0136D22	11	7.9	29	28	AZ335439	1M0065F24
247	11.2	8.1	29	28	AZ985140	2M0266H20	AZ985140	2M0266H20	11	7.9	29	28	AZ342886	1M0076R06
248	11.2	8.1	29	28	BH907056	SALK_0378	BH907056	SALK_0378	11	7.9	29	28	AZ387818	1M0147C20
249	11.2	8.1	29	29	CC457201	SALK_1072	CC457201	SALK_1072	11	7.9	29	28	AZ495577	1M0331F03
250	11.2	8.1	29	29	TA263B02P	AL483789 T. brucei	AL483789	T. brucei	11	7.9	29	28	AZ694094	AST-2HB8G
251	11.2	8.1	30	9	AU244302	AU244302	AU244302		11	7.9	29	28	AZ833405	2M0115P19
252	11.2	8.1	30	10	BE277260	601178250	BE277260	601178250	11	7.9	29	28	AZ950714	2M0214I20
253	11.2	8.1	30	10	BE295129	601173573	BE295129	601173573	11	7.9	29	28	BH023787	BG02425-5
254	11.2	8.1	30	10	BE295129	601173573	BE295129	601173573	11	7.9	29	28	BH023787	BG02425-5
255	11.2	8.1	30	10	BE378923	601237514	BE378923	601237514	11	7.9	29	28	BH791186	SALK_0588
256	11.2	8.1	30	10	BE559533	601345383	BE559533	601345383	11	7.9	29	28	BH863568	SALK_0941
257	11.2	8.1	30	12	B1222858	602941108	B1222858	602941108	11	7.9	29	28	BH909372	SALK_0532
258	11.2	8.1	30	28	AZ323517	1M0045A04	AZ323517	1M0045A04	11	7.9	29	28	TA133D12P	AL465919 T. brucei
259	11.2	8.1	30	28	AZ337154	1M0067B11	AZ337154	1M0067B11	11	7.9	30	10	BE727754	601564575
260	11.2	8.1	30	28	AZ343221	1M0076K02	AZ343221	1M0076K02	11	7.9	30	28	AZ360543	1M0103004
261	11.2	8.1	30	28	AZ416610	1M0152L06	AZ416610	1M0152L06	11	7.9	30	28	AZ811507	2M0077K08
262	11.2	8.1	30	28	AZ588957	1M0397B08	AZ588957	1M0397B08	11	7.9	30	28	AZ958796	2M0226C14
263	11.2	8.1	30	28	AZ591789	1M0402P06	AZ591789	1M0402P06	11	7.9	30	28	BH850662	SALK_0973
264	11.2	8.1	30	28	AZ783946	2M0036B08	AZ783946	2M0036B08	11	7.9	30	29	AL761633	Arabidops
265	11.2	8.1	30	28	AZ787677	2M0034H17	AZ787677	2M0034H17	11	7.9	30	29	DR31G1T	AL9761633
266	11.2	8.1	30	28	AZ810546	2M0076F10	AZ810546	2M0076F10	11	7.9	30	29	DR35M6T	AL978457 Danio rer
267	11.2	8.1	30	28	AZ824893	2M0099H17	AZ824893	2M0099H17	11	7.9	30	29	DR43B12S	AL979145 Danio rer
268	11.2	8.1	30	28	AZ827938	2M0104J09	AZ827938	2M0104J09	11	7.9	30	28	AZ662892	1M0542D15
269	11.2	8.1	19	28	AZ795136	2M0049A16	AZ795136	2M0049A16	10.8	7.8	19	28	AZ835034	2M0129K04
270	11	7.9	20	28	AZ445379	1M0241E07	AZ445379	1M0241E07	10.8	7.8	20	28	AZ317291	1M0035N10
271	11	7.9	20	28	AZ811106	2M0077P03	AZ811106	2M0077P03	10.8	7.8	20	28	AZ591658	1M0401F19
272	11	7.9	21	28	AZ509602	1M0352E08	AZ509602	1M0352E08	10.8	7.8	21	28	AZ766315	1M0563K14
273	11	7.9	22	9	A1439277	t154a02.x	A1439277	t154a02.x	10.8	7.8	22	9	AA894572	AA894572 of91g02.r
274	11	7.9	22	28	AZ478594	1M0298I15	AZ478594	1M0298I15	10.8	7.8	22	9	A1354432	qul17d02.x
275	11	7.9	22	28	AZ640656	1M0502K14	AZ640656	1M0502K14	10.8	7.8	22	14	D21051	HUNGSO2036
276	11	7.9	22	28	AZ779122	2M0015M03	AZ779122	2M0015M03	10.8	7.8	22	28	AZ876923	2M0192D07
277	11	7.9	22	28	AZ787955	2M0034E18	AZ787955	2M0034E18	10.8	7.8	23	12	BM392543	50071-2-1
278	11	7.9	22	28	AZ892662	2M0263J06	AZ892662	2M0263J06	10.8	7.8	23	12	BM393611	50072-2-1
279	11	7.9	22	28	TA110C02Q	AL461782 T. brucei	AL461782	T. brucei	10.8	7.8	23	14	L32041	HUMXP2D9B H
280	11	7.9	23	28	AZ308569	1M0011M08	AZ308569	1M0011M08	10.8	7.8	23	28	AZ303987	1M0033H22
281	11	7.9	23	28	AZ331549	1M0059K02	AZ331549	1M0059K02	10.8	7.8	23	28	AZ443442	1M0238E16
282	11	7.9	23	28	AZ435508	1M0080I01	AZ435508	1M0080I01	10.8	7.8	23	28	AZ594286	1M0406H11
283	11	7.9	23	28	AZ470241	1M0284B16	AZ470241	1M0284B16	10.8	7.8	23	28	AZ759994	1M0553N14
284	11	7.9	23	28	AZ627985	1M0476O06	AZ627985	1M0476O06	10.8	7.8	23	28	AZ819914	2M0091N16
285	11	7.9	23	28	AZ785457	2M0039A24	AZ785457	2M0039A24	10.8	7.8	23	28	AZ871545	2M0184A04
286	11	7.9	23	28	AZ785926	2M0030K08	AZ785926	2M0030K08	10.8	7.8	23	29	TA61D03Q	AL456207 T. brucei
287	11	7.9	23	28	AZ970753	2M0244E01	AZ970753	2M0244E01	10.8	7.8	24	12	BM392455	50071-2-1
288	11	7.9	24	28	AZ449706	1M0248M02	AZ449706	1M0248M02	10.8	7.8	24	12	BM393436	50072-2-1
289	11	7.9	24	28	AZ455814	1M0258B21	AZ455814	1M0258B21	10.8	7.8	24	12	AZ309247	1M0013114
290	11	7.9	24	28	AZ621109	1M0454D12	AZ621109	1M0454D12	10.8	7.8	24	28	AZ374682	1M0127B12
291	11	7.9	24	28	AZ825943	2M0101H19	AZ825943	2M0101H19	10.8	7.8	24	28	AZ655394	1M0530C05
292	11	7.9	24	29	BZ290658	SALK_0908	BZ290658	SALK_0908	10.8	7.8	24	28	AZ815479	2M0083D15
293	11	7.9	25	9	A1025765	ov94a03.s	A1025765	ov94a03.s	10.8	7.8	24	28	AZ826609	2M0102F18
294	11	7.9	25	28	AZ620092	1M0452J07	AZ620092	1M0452J07	10.8	7.8	24	28	BH910704	SALK_0614
295	11	7.9	25	28	AZ774118	2M0003K08	AZ774118	2M0003K08	10.8	7.8	24	29	BZ356062	1M023012
296	11	7.9	26	28	AZ345607	1M0080C20	AZ345607	1M0080C20	10.8	7.8	25	9	A1023012	ow57f01.r

us-09-925-139-3_copy_1631_1769.max.rst

Mon Aug 25 09:45:55 2003

C 370	10.8	7.8	25	9	AI155015	AI155015 ud79a02.r	443	10.6	7.6	19	28	AZ761834	AZ761834
C 371	10.8	7.8	25	9	AI361952	AI361952 QY37E02.x	C 444	10.6	7.6	20	28	AZ308179	AZ308179
C 372	10.8	7.8	25	9	AI363940	AI363940 QW34B12.x	C 445	10.6	7.6	20	28	AZ333215	AZ333215
C 373	10.8	7.8	25	12	BI094828	BI094828 EST-CD34N	C 446	10.6	7.6	20	28	AZ333930	AZ333930
C 374	10.8	7.8	25	12	BI094828	BI094828 5009-0-2-	C 447	10.6	7.6	20	28	AZ423776	AZ423776
C 375	10.8	7.8	25	14	CO0104	CO0104 HUNG0000572	C 448	10.6	7.6	20	28	AZ5292780	AZ5292780
C 376	10.8	7.8	25	28	AZ584819	AZ584819 LM0389A13	C 449	10.6	7.6	20	28	AZ601843	AZ601843
C 377	10.8	7.8	25	28	AZ588162	AZ588162 LM0396K07	C 450	10.6	7.6	20	28	AZ658035	AZ658035
C 378	10.8	7.8	25	28	AZ803224	AZ803224 LM0396K07	C 451	10.6	7.6	20	28	AZ833186	AZ833186
C 379	10.8	7.8	25	28	AZ810739	AZ810739 LM0396K07	C 452	10.6	7.6	20	28	AZ833505	AZ833505
C 380	10.8	7.8	25	28	AZ938825	AZ938825 LM0396K07	C 453	10.6	7.6	20	28	AI472050	AI472050
C 381	10.8	7.8	25	14	T61018	T61018 YB74B11.r1	C 454	10.6	7.6	21	9	AU254493	AU254493
C 382	10.8	7.8	26	28	AZ320242	AZ320242 LM0040M12	C 455	10.6	7.6	21	28	AZ626594	AZ626594
C 383	10.8	7.8	26	28	AZ449518	AZ449518 LM0247K13	C 456	10.6	7.6	21	28	AZ758704	AZ758704
C 384	10.8	7.8	26	28	AZ459978	AZ459978 LM0265F07	C 457	10.6	7.6	22	9	AI183338	AI183338
C 385	10.8	7.8	26	28	AZ779432	AZ779432 LM0015P14	C 458	10.6	7.6	22	9	AI441822	AI441822
C 386	10.8	7.8	26	29	BZ353740	BZ353740 SALK_1220	C 459	10.6	7.6	22	14	D21051	D21051
C 387	10.8	7.8	26	29	BZ384018	BZ384018 SALK_1349	C 460	10.6	7.6	23	28	AZ333934	AZ333934
C 388	10.8	7.8	27	12	BM396690	BM396690 5009-0-24	C 461	10.6	7.6	23	28	AZ416800	AZ416800
C 389	10.8	7.8	27	12	BM396690	BM396690 5009-0-24	C 462	10.6	7.6	23	28	AZ450507	AZ450507
C 390	10.8	7.8	27	28	AZ418585	AZ418585 LM0194A18	C 463	10.6	7.6	23	28	AZ822792	AZ822792
C 391	10.8	7.8	27	28	AZ418585	AZ418585 SALK_1031	C 464	10.6	7.6	23	28	AZ822965	AZ822965
C 392	10.8	7.8	27	29	BZ593155	BZ593155 SALK_0622	C 465	10.6	7.6	23	28	AZ979817	AZ979817
C 393	10.8	7.8	27	29	AZ226118	AZ226118 Lotus_jap	C 466	10.6	7.6	23	28	BH903843	BH903843
C 394	10.8	7.8	27	29	TA292F02P	TA292F02P	C 467	10.6	7.6	23	29	TA380G08Q	TA380G08Q
C 395	10.8	7.8	28	9	AI376644	AI376644 te63b01.x	C 468	10.6	7.6	24	28	AZ623720	AZ623720
C 396	10.8	7.8	28	9	AI522573	AI522573 fb59d12.x	C 469	10.6	7.6	24	28	AZ658406	AZ658406
C 397	10.8	7.8	28	9	AI677996	AI677996 wc81e09.x	C 470	10.6	7.6	24	28	AZ800644	AZ800644
C 398	10.8	7.8	28	12	BM393660	BM393660 50072-2-1	C 471	10.6	7.6	25	9	AA881443	AA881443
C 399	10.8	7.8	28	12	BM393660	BM393660 50071-2-1	C 472	10.6	7.6	25	9	AI138565	AI138565
C 400	10.8	7.8	28	14	H14469	H14469 YL25H01.r1	C 473	10.6	7.6	25	12	BG292523	BG292523
C 401	10.8	7.8	28	28	AQ026271	AQ026271 1(3)L6241	C 474	10.6	7.6	25	13	BQ584791	BQ584791
C 402	10.8	7.8	28	28	AZ456558	AZ456558 LM0080M22	C 475	10.6	7.6	25	13	BQ589704	BQ589704
C 403	10.8	7.8	28	28	AZ480483	AZ480483 LM0302J04	C 476	10.6	7.6	25	14	N32966	N32966
C 404	10.8	7.8	28	28	AZ806070	AZ806070 LM0067G21	C 477	10.6	7.6	25	28	AZ364139	AZ364139
C 405	10.8	7.8	28	28	AZ811033	AZ811033 LM0077B02	C 478	10.6	7.6	25	28	AZ472671	AZ472671
C 406	10.8	7.8	28	28	BH908006	BH908006 SALK_0451	C 479	10.6	7.6	25	28	AZ776661	AZ776661
C 407	10.8	7.8	28	28	BM392636	BM392636 50071-2-1	C 480	10.6	7.6	25	28	AZ824843	AZ824843
C 408	10.8	7.8	29	12	BM392636	BM392636 50071-2-1	C 481	10.6	7.6	25	28	AZ873581	AZ873581
C 409	10.8	7.8	29	12	BM393364	BM393364 50071-2-9	C 482	10.6	7.6	25	29	TA208E01Q	TA208E01Q
C 410	10.8	7.8	29	12	BM393364	BM393364 50072-2-1	C 483	10.6	7.6	25	29	TA393F07P	TA393F07P
C 411	10.8	7.8	29	12	BM393805	BM393805 50072-2-1	C 484	10.6	7.6	26	28	AZ309096	AZ309096
C 412	10.8	7.8	29	12	BM393805	BM393805 50072-2-9	C 485	10.6	7.6	26	28	AZ466526	AZ466526
C 413	10.8	7.8	29	14	CA797153	CA797153 Cac_BL_42	C 486	10.6	7.6	26	28	BH901105	BH901105
C 414	10.8	7.8	29	14	N85094	N85094 J2291F Huma	C 487	10.6	7.6	26	29	CO56638	CO56638
C 415	10.8	7.8	29	28	AZ332711	AZ332711 LM0061N14	C 488	10.6	7.6	27	14	R07762	R07762
C 416	10.8	7.8	29	28	AZ335439	AZ335439 LM0065P24	C 489	10.6	7.6	27	14	T79181	T79181
C 417	10.8	7.8	29	28	AZ387832	AZ387832 LM0147P23	C 490	10.6	7.6	27	28	AZ308445	AZ308445
C 418	10.8	7.8	29	28	AZ440659	AZ440659 LM0231015	C 491	10.6	7.6	27	28	AZ768325	AZ768325
C 419	10.8	7.8	29	28	AZ588337	AZ588337 LM0396P01	C 492	10.6	7.6	27	28	AZ801860	AZ801860
C 420	10.8	7.8	29	28	AZ633359	AZ633359 LM0488K02	C 493	10.6	7.6	27	28	AZ827063	AZ827063
C 421	10.8	7.8	29	28	AZ636336	AZ636336 LM0495D12	C 494	10.6	7.6	27	28	AZ863555	AZ863555
C 422	10.8	7.8	29	28	BH759297	BH759297 KG01248-3	C 495	10.6	7.6	27	28	BZ356916	BZ356916
C 423	10.8	7.8	29	28	BH84492	BH84492 SALK_0961	C 496	10.6	7.6	27	29	BZ356916	BZ356916
C 424	10.8	7.8	29	29	BH84492	BH84492 SALK_1301	C 497	10.6	7.6	27	29	TA308E12P	TA308E12P
C 425	10.8	7.8	29	29	TA18E08P	TA18E08P	C 498	10.6	7.6	27	29	TA339A01Q	TA339A01Q
C 426	10.8	7.8	29	29	TA225F03P	TA225F03P	C 499	10.6	7.6	27	29	TA344E01P	TA344E01P
C 427	10.8	7.8	30	10	BE297610	BE297610 601178187	C 500	10.6	7.6	28	9	AA856526	AA856526
C 428	10.8	7.8	30	12	BM393328	BM393328 50071-2-9	C 501	10.6	7.6	28	9	AA863634	AA863634
C 429	10.8	7.8	30	12	BM395411	BM395411 50072-2-9	C 502	10.6	7.6	28	9	AA940225	AA940225
C 430	10.8	7.8	30	12	BM395430	BM395430 50072-2-9	C 503	10.6	7.6	28	9	AA990155	AA990155
C 431	10.8	7.8	30	14	D12308	D12308 HUM0005631	C 504	10.6	7.6	28	9	AA996369	AA996369
C 432	10.8	7.8	30	28	AZ408503	AZ408503 LM0179P12	C 505	10.6	7.6	28	9	AA996369	AA996369
C 433	10.8	7.8	30	28	AZ458683	AZ458683 LM0263D03	C 506	10.6	7.6	28	9	AA996369	AA996369
C 434	10.8	7.8	30	28	AZ471850	AZ471850 LM0286M08	C 507	10.6	7.6	28	9	AA996369	AA996369
C 435	10.8	7.8	30	28	AZ474529	AZ474529 LM0292B13	C 508	10.6	7.6	28	9	AA996369	AA996369
C 436	10.8	7.8	30	28	AZ634665	AZ634665 LM0490P02	C 509	10.6	7.6	28	9	AA996369	AA996369
C 437	10.8	7.8	30	28	AZ666770	AZ666770 LM0549G08	C 510	10.6	7.6	28	9	AA996369	AA996369
C 438	10.8	7.8	30	28	AZ666770	AZ666770 LM0549G08	C 511	10.6	7.6	28	14	CA795841	CA795841
C 439	10.8	7.8	30	28	AZ792571	AZ792571 LM0045D12	C 512	10.6	7.6	28	28	AZ303959	AZ303959
C 440	10.8	7.8	30	28	AZ792571	AZ792571 LM0045D12	C 513	10.6	7.6	28	28	AZ327470	AZ327470
C 441	10.6	7.6	19	28	AZ307462	AZ307462 LM0009I08	C 514	10.6	7.6	28	28	AZ489682	AZ489682
C 442	10.6	7.6	19	28	AZ346707	AZ346707 LM0082M04	C 515	10.6	7.6	28	28	AZ511067	AZ511067

C 516	10.6	7.6	28	28	AZ512393	1M0357F20	589	10.4	7.5	24	28	AZ505513	1M0346B13
C 517	10.6	7.6	28	28	AZ590898	1M0400A16	590	10.4	7.5	24	28	AZ761059	1M0555L08
C 518	10.6	7.6	28	28	AZ836785	2M0131I14	C 591	10.4	7.5	24	28	AZ796057	2M0051B13
C 519	10.6	7.6	28	28	AZ842146	2M0140D04	C 592	10.4	7.5	24	28	AZ817421	2M0086L12
C 520	10.6	7.6	28	28	AZ974910	2M0249E15	C 593	10.4	7.5	24	28	AZ983288	2M0264G23
C 521	10.6	7.6	28	28	AZ246945	2822529.5	C 594	10.4	7.5	24	29	TA349806Q	2M0264G23
C 522	10.6	7.6	28	28	BM395134	50072-2-7	C 595	10.4	7.5	25	9	AU254124	TA349806Q
C 523	10.6	7.6	28	28	AZ307046	1M0008E24	C 596	10.4	7.5	25	12	BM395408	AU254124
C 524	10.6	7.6	28	28	AZ331636	1M0059O09	C 597	10.4	7.5	25	12	BM396165	50072-2-8
C 525	10.6	7.6	28	28	AZ345862	1M0080I14	C 598	10.4	7.5	25	12	AZ483610	5009-0-18
C 526	10.6	7.6	28	28	AZ398458	1M0163D21	C 599	10.4	7.5	25	28	AZ483610	1M0309N21
C 527	10.6	7.6	28	28	AZ427756	1M0209O20	C 600	10.4	7.5	25	28	AZ510562	1M0355F11
C 528	10.6	7.6	28	28	AZ430267	1M0214K11	C 601	10.4	7.5	25	28	AZ513486	1M0359A04
C 529	10.6	7.6	28	28	AZ432529	1M0218C04	C 602	10.4	7.5	25	28	AZ513486	1M0359A04
C 530	10.6	7.6	28	28	AZ642459	1M0505D06	C 603	10.4	7.5	25	28	AZ588253	1M0396O23
C 531	10.6	7.6	28	28	AZ780387	2M0017N12	C 604	10.4	7.5	25	28	AZ621312	1M0454F19
C 532	10.6	7.6	28	28	AZ815922	2M0084L06	C 605	10.4	7.5	25	28	AZ834056	2M0092O01
C 533	10.6	7.6	28	28	AZ820565	2M0092A22	C 606	10.4	7.5	25	28	AZ943422	2M0204P06
C 534	10.6	7.6	28	28	AZ838807	2M0106J03	C 607	10.4	7.5	25	28	BH40574	KG05441-5
C 535	10.6	7.6	28	28	AZ998267	2M0285D12	C 608	10.4	7.5	25	28	BH863402	SALK_0938
C 536	10.6	7.6	30	14	C01081		C 609	10.4	7.5	25	28	BH865143	SALK_0974
C 537	10.6	7.6	30	14	C01081		C 610	10.4	7.5	25	29	BH865143	SALK_0974
C 538	10.6	7.6	30	28	AZ408639	1M0179I23	C 611	10.4	7.5	25	29	TA111D05P	AL461854 T. brucei
C 539	10.6	7.6	30	28	AZ408639	1M0179I23	C 612	10.4	7.5	25	29	TA263P03Q	AL461854 T. brucei
C 540	10.6	7.6	30	28	AZ597778	1M0367I16	C 613	10.4	7.5	26	28	AZ309024	1M0026D12
C 541	10.6	7.6	30	28	AZ587961	1M0396B06	C 614	10.4	7.5	26	28	AZ333183	1M0062D12
C 542	10.6	7.6	30	28	AZ657672	1M0534G02	C 615	10.4	7.5	26	28	AZ783529	2M0025D24
C 543	10.6	7.6	30	28	AZ658443	1M0535F23	C 616	10.4	7.5	26	28	AZ864944	2M0174M17
C 544	10.6	7.6	30	28	AZ783604	2M0025F05	C 617	10.4	7.5	26	28	AZ949204	2M0212M04
C 545	10.6	7.6	30	28	AZ801555	2M0060M01	C 618	10.4	7.5	26	28	AZ969979	2M0242024
C 546	10.6	7.6	30	28	AZ941284	2M0201A02	C 619	10.4	7.5	26	28	BH863961	SALK_0949
C 547	10.6	7.6	30	28	BH850114	SALK_0708	C 620	10.4	7.5	26	28	CC060543	CC060543
C 548	10.6	7.6	30	28	BZ355049	SALK_1262	C 621	10.4	7.5	26	28	AZ355810	1M0095G10
C 549	10.6	7.6	30	29	AG230564	Lotus_jap	C 622	10.4	7.5	27	28	AZ357559	1M0099L09
C 550	10.6	7.6	30	29	DR31G1T		C 623	10.4	7.5	27	28	AZ495213	1M0331A04
C 551	10.4	7.5	20	13	BM395025	50072-2-7	C 624	10.4	7.5	27	28	AZ594886	1M0407D12
C 552	10.4	7.5	20	13	BQ586354	E012395-0	C 625	10.4	7.5	27	28	AZ5813093	2M0080O08
C 553	10.4	7.5	20	28	AZ345442		C 626	10.4	7.5	27	28	AZ830284	2M0109N21
C 554	10.4	7.5	20	28	AZ393773		C 627	10.4	7.5	28	9	AA902937	OK45903.s
C 555	10.4	7.5	20	28	AZ827586	2M0104C08	C 628	10.4	7.5	28	9	AA937308	OM16H06.s
C 556	10.4	7.5	21	12	BG896906	HOA59-1-A	C 629	10.4	7.5	28	9	AI006239	ua88611.r
C 557	10.4	7.5	21	28	AZ313243	1M0029H16	C 630	10.4	7.5	28	9	AI019322	ub18g12.r
C 558	10.4	7.5	21	28	AZ348213	1M0084N15	C 631	10.4	7.5	28	9	AI153397	uc52e05.r
C 559	10.4	7.5	21	28	AZ359241		C 632	10.4	7.5	28	9	AI686757	cx09502.x
C 560	10.4	7.5	21	28	AZ430565	1M0102D03	C 633	10.4	7.5	28	9	AI744403	cx09502.x
C 561	10.4	7.5	21	28	AZ442098	1M0234F12	C 634	10.4	7.5	28	13	BQ593191	E012795-0
C 562	10.4	7.5	21	28	AZ445481	1M0241P15	C 635	10.4	7.5	28	28	AQ025041	EP(2)1164
C 563	10.4	7.5	21	28	AZ595699	1M0408C02	C 636	10.4	7.5	28	28	AZ309062	1M0012B14
C 564	10.4	7.5	21	28	AZ610251	1M0435M21	C 637	10.4	7.5	28	28	AZ619085	1M0451R14
C 565	10.4	7.5	21	28	AZ783428	2M0025F10	C 638	10.4	7.5	28	28	AZ632301	1M0486G23
C 566	10.4	7.5	21	28	AZ817003	2M0086C04	C 639	10.4	7.5	28	28	AZ811033	2M0077B02
C 567	10.4	7.5	22	28	AZ334102	1M0063B16	C 640	10.4	7.5	28	28	AZ839856	2M0136L08
C 568	10.4	7.5	22	28	AZ430045	1M0214O17	C 641	10.4	7.5	28	28	AZ835955	2M0156D23
C 569	10.4	7.5	22	28	AZ479083	2M0299F03	C 642	10.4	7.5	28	28	BH855787	BH855787 SALK_0845
C 570	10.4	7.5	22	28	AZ579287	1M0363K11	C 643	10.4	7.5	28	29	BZ291486	SALK_1208
C 571	10.4	7.5	22	28	AZ612552	1M0439G12	C 644	10.4	7.5	28	29	BZ664334	SALK_0699
C 572	10.4	7.5	22	28	AZ631537	1M0485F17	C 645	10.4	7.5	29	14	RJ1895	Yh60d10.r
C 573	10.4	7.5	22	28	AZ711198	1M0573M08	C 646	10.4	7.5	29	28	AZ580321	1M0368G02
C 574	10.4	7.5	22	28	AZ813877	2M0081P13	C 647	10.4	7.5	29	28	AZ769743	1M0570C15
C 575	10.4	7.5	23	10	BG668141	DRABWE02	C 648	10.4	7.5	29	28	AZ771858	1M0574P16
C 576	10.4	7.5	23	28	AZ334719	1M0064P07	C 649	10.4	7.5	29	28	AZ788256	2M0035A17
C 577	10.4	7.5	23	28	AZ374746	1M0127D15	C 650	10.4	7.5	29	28	AZ834401	2M0117P03
C 578	10.4	7.5	23	28	AZ387189	1M0146L24	C 651	10.4	7.5	29	28	BH848482	BH848482 SALK_0684
C 579	10.4	7.5	23	28	AZ480676	1M0302F23	C 652	10.4	7.5	29	28	BH856361	BH856361 SALK_0798
C 580	10.4	7.5	23	28	AZ610143	1M0435H17	C 653	10.4	7.5	29	29	CC057376	SALK_1410
C 581	10.4	7.5	23	28	AZ610186	1M0435A21	C 654	10.4	7.5	29	29	TA225F03P	AL479925 T. brucei
C 582	10.4	7.5	23	28	AZ646716	1M0512D23	C 655	10.4	7.5	30	2	HS007697	AL042847 Homo sapi
C 583	10.4	7.5	23	28	AZ663880	1M0543D14	C 656	10.4	7.5	30	10	BE279576	BE279576 601157461
C 584	10.4	7.5	23	28	AZ784963	2M0028F20	C 657	10.4	7.5	30	10	BE384678	BE384678 601276956
C 585	10.4	7.5	23	28	AZ863841	2M0173F09	C 658	10.4	7.5	30	10	BE729410	BE729410 601561442
C 586	10.4	7.5	24	14	D18741		C 659	10.4	7.5	30	12	BI463777	BI463777 603203487
C 587	10.4	7.5	24	28	AZ404465	1M0172P09	C 660	10.4	7.5	30	12	BI521544	BI521544 603081368
C 588	10.4	7.5	24	28	AZ437306	1M0225D03	C 661	10.4	7.5	30	14	U41135	U41135 ENU41135 A8

808	10.2	7.3	28	29	BZ380400	SALK_1150	C 881	10	7.2	19	28	AZ819577	AZ819577	2M0091H18
809	10.2	7.3	28	29	TA146H09P	AL47405 T. Bruce1	882	10	7.2	19	28	AZ859728	AZ859728	2M0165M22
C 810	10.2	7.3	29	9	AU258464	AU258464	883	10	7.2	19	28	AZ962769	AZ962769	2M0231P08
C 811	10.2	7.3	29	9	AU263780	AU263780	884	10	7.2	19	28	BM393606	BM393606	50072-2-1
812	10.2	7.3	29	14	T50325	YB24f01_x1	C 885	10	7.2	20	12	BM393606	BM393606	50072-2-1
813	10.2	7.3	29	28	AZ398458	1M0163D21	886	10	7.2	20	13	BM393606	BM393606	50072-2-1
814	10.2	7.3	29	28	AZ414668	1M0185M20	887	10	7.2	20	28	AZ318416	AZ318416	1M0037P19
815	10.2	7.3	29	28	AZ449708	1M0248M04	888	10	7.2	20	28	AZ333707	AZ333707	1M0067K23
816	10.2	7.3	29	28	AZ475726	1M0294F02	C 889	10	7.2	20	28	AZ427744	1M0209L23	AZ427744
C 817	10.2	7.3	29	28	AZ661923	1M0540C13	C 889	10	7.2	20	28	AZ430735	1M0215A22	AZ430735
C 818	10.2	7.3	29	28	AZ761188	1M0555E21	C 890	10	7.2	20	28	AZ492125	1M0326L05	AZ492125
C 819	10.2	7.3	29	28	AZ780173	2M0017H18	C 891	10	7.2	20	28	AZ590476	1M0400F06	AZ590476
C 820	10.2	7.3	29	28	AZ795441	2M0049K12	C 892	10	7.2	20	28	AZ652975	1M0526L20	AZ652975
C 821	10.2	7.3	29	28	AZ851520	2M0153J18	C 893	10	7.2	21	28	AZ321746	1M0042N20	AZ321746
C 822	10.2	7.3	29	28	AZ966795	2M0237P23	894	10	7.2	21	28	AZ345432	1M0080D07	AZ345432
C 823	10.2	7.3	29	28	AZ973455	2M0247M08	895	10	7.2	21	28	AZ345433	1M0080D12	AZ345433
C 824	10.2	7.3	29	28	AZ995806	2M0281G17	896	10	7.2	21	28	AZ492483	1M00326F07	AZ492483
C 825	10.2	7.3	29	28	AQ254876	EP(2)2583	C 897	10	7.2	21	28	AZ609594	1M0434M18	AZ609594
826	10.2	7.3	29	28	BH754390	SALK_0412	898	10	7.2	21	28	AZ816467	2M0085B14	AZ816467
827	10.2	7.3	29	28	BH812547	SALK_0619	899	10	7.2	21	28	AZ967090	2M0237D24	AZ967090
828	10.2	7.3	29	29	BZ352777	SALK_0822	C 900	10	7.2	22	9	A1183338	qd41a12_x	A1183338
829	10.2	7.3	29	29	BZ353826	SALK_1222	C 901	10	7.2	22	9	A1631347	tz83c04_x	A1631347
830	10.2	7.3	29	29	BZ381809	SALK_1173	902	10	7.2	22	9	A1700139	tg10h09_x	A1700139
831	10.2	7.3	29	29	BZ382190	SALK_1179	903	10	7.2	22	28	AZ316190	1M0033C18	AZ316190
832	10.2	7.3	29	29	BZ382516	SALK_1184	904	10	7.2	22	28	AZ396435	1M0161C03	AZ396435
833	10.2	7.3	29	29	BZ383220	SALK_1252	905	10	7.2	22	28	AZ492512	1M0326K08	AZ492512
834	10.2	7.3	29	29	BZ383311	SALK_1324	906	10	7.2	22	28	AZ821337	2M0094L04	AZ821337
835	10.2	7.3	29	29	TA38G11P	AL453566 T. Bruce1	C 907	10	7.2	22	28	AZ828663	2M0105T14	AZ828663
C 836	10.2	7.3	30	9	AU255782	AU255782	C 908	10	7.2	22	28	AZ839610	2M0135M17	AZ839610
C 837	10.2	7.3	30	10	BE278221	601180085	909	10	7.2	22	28	AZ851620	2M0153M24	AZ851620
C 838	10.2	7.3	30	10	BE278715	601158914	910	10	7.2	22	28	AZ942905	2M0203K13	AZ942905
C 839	10.2	7.3	30	10	BE378923	601237514	C 911	10	7.2	22	29	TA197A09Q	AL477177 T. Bruce1	AL477177
840	10.2	7.3	30	10	BE384364	601277465	C 912	10	7.2	22	29	TA197A09Q	AL477177 T. Bruce1	AL477177
C 841	10.2	7.3	30	10	BE385997	601276651	913	10	7.2	23	12	BM394013	50072-2-1	BM394013
C 842	10.2	7.3	30	10	BE386027	601276707	C 914	10	7.2	23	28	AZ335717	1M0065J20	AZ335717
C 843	10.2	7.3	30	10	BE386094	601276796	915	10	7.2	23	28	AZ336293	1M0066E02	AZ336293
C 844	10.2	7.3	30	10	BE386454	601289369	C 915	10	7.2	23	28	AZ433756	1M0219U18	AZ433756
C 845	10.2	7.3	30	10	BE561270	601344283	C 917	10	7.2	23	28	AZ459779	1M0264A22	AZ459779
C 846	10.2	7.3	30	10	BE727754	601564575	918	10	7.2	23	28	AZ586739	1M0392J21	AZ586739
C 847	10.2	7.3	30	10	BE741581	601594894	C 919	10	7.2	23	28	AZ613963	1M0442K06	AZ613963
C 848	10.2	7.3	30	12	BM396162	5009-0-18	920	10	7.2	23	28	AZ647317	1M0513F14	AZ647317
C 849	10.2	7.3	30	12	BM397741	5009-0-36	921	10	7.2	23	28	AZ782422	2M0022E17	AZ782422
C 850	10.2	7.3	30	14	N23450	YV99e07_81	C 922	10	7.2	23	28	AZ973344	2M0247H06	AZ973344
C 851	10.2	7.3	30	28	AZ309878	AZ309878	C 923	10	7.2	23	29	BZ352393	SAUK_0789	BZ352393
C 852	10.2	7.3	30	28	AZ318451	1M0037L05	C 924	10	7.2	23	29	BZ765371	SAUK_1309	BZ765371
C 853	10.2	7.3	30	28	AZ357485	1M0099G05	C 925	10	7.2	23	29	TA369A11Q	SAUK_1309	TA369A11Q
854	10.2	7.3	30	28	AZ424992	1M0204B24	926	10	7.2	24	28	AZ309633	1M0016B22	AZ309633
855	10.2	7.3	30	28	AZ431599	1M0216C12	927	10	7.2	24	28	AZ343358	1M0076A14	AZ343358
856	10.2	7.3	30	28	AZ437578	1M0225T24	928	10	7.2	24	28	AZ437010	1M0082T04	AZ437010
C 857	10.2	7.3	30	28	AZ441270	1M0232G19	C 929	10	7.2	24	28	AZ408805	1M0180B01	AZ408805
C 858	10.2	7.3	30	28	AZ510129	1M0354L24	930	10	7.2	24	28	AZ428114	1M0210A01	AZ428114
859	10.2	7.3	30	28	AZ613059	1M0441D13	C 931	10	7.2	24	28	AZ437306	1M0225D03	AZ437306
C 860	10.2	7.3	30	28	AZ634665	1M0490P02	C 932	10	7.2	24	28	AZ47502	2M0148C08	AZ47502
C 861	10.2	7.3	30	28	AZ654936	1M0529M06	933	10	7.2	25	9	AA931385	oo03f05_s	AA931385
C 862	10.2	7.3	30	28	AZ782713	2M0023M21	934	10	7.2	25	9	AA988825	or85f11_s	AA988825
C 863	10.2	7.3	30	28	AZ788197	2M0035F12	C 935	10	7.2	25	9	AA994917	ou21d04_s	AA994917
C 864	10.2	7.3	30	28	AZ987528	2M0270E08	C 936	10	7.2	25	9	AA164044	ue73e05_r	AA164044
865	10.2	7.3	30	29	BZ354478	SALK_1251	C 937	10	7.2	25	9	AA164044	ue73e05_r	AA164044
866	10.2	7.3	30	29	BZ354508	SALK_1252	C 938	10	7.2	25	9	AU256355	AU256355	AU256355
867	10.2	7.3	30	29	BZ382499	SALK_1183	939	10	7.2	25	14	L32049	HUMXP428A_H	L32049
868	10.2	7.3	30	29	BZ383490	SALK_1340	940	10	7.2	25	28	AZ436428	1M0224K10	AZ436428
869	10.2	7.3	30	29	BZ594398	SALK_0840	941	10	7.2	25	28	AZ490888	1M0324G10	AZ490888
870	10.2	7.3	30	29	C457477	CC457477	C 942	10	7.2	25	28	AZ511615	1M0356B14	AZ511615
871	10.2	7.3	30	29	AG230072	Lotus Jap	943	10	7.2	25	28	AZ579573	1M0367M05	AZ579573
C 872	10.2	7.3	30	29	CNS07HV6	AL611556 Anopheles	C 944	10	7.2	25	28	AZ580365	1M0368002	AZ580365
C 873	10.2	7.3	30	29	HSNC06B01	X88548 H. sapiens D	945	10	7.2	25	28	AZ780039	2M0016P21	AZ780039
874	10.2	7.2	19	9	AT016864	ou27c11_x	C 946	10	7.2	25	28	AZ794198	2M0047D20	AZ794198
C 875	10.2	7.2	19	12	BM395903	5009-0-13	947	10	7.2	25	28	AZ795988	2M0051H07	AZ795988
C 876	10.2	7.2	19	28	AZ343228	1M0076M05	948	10	7.2	25	28	AZ832353	2M0112011	AZ832353
C 877	10.2	7.2	19	28	AZ410166	1M0182J17	C 949	10	7.2	25	28	BH852665	SAUK_0754	BH852665
878	10.2	7.2	19	28	AZ579189	1M0363I12	950	10	7.2	25	29	BZ381778	SAUK_1172	BZ381778
879	10.2	7.2	19	28	AZ586043	1M0391L12	951	10	7.2	25	29	BZ383219	SAUK_1252	BZ383219
C 880	10.2	7.2	19	28	AZ775540	2M0008H15	952	10	7.2	25	29	BZ383316	SAUK_1324	BZ383316
							C 953	10	7.2	25	29	BZ597082	SAUK_0993	BZ597082

c 954	10	7.2	25	29	BZ765313	SALK_1300
c 955	10	7.2	25	29	AL461854	T. brucei
c 956	10	7.2	25	29	AL478330	T. brucei
c 957	10	7.2	26	14	H53363	yc86g08.s1
c 958	10	7.2	26	14	T60922	yc46d07.s1
c 959	10	7.2	26	28	AZ314210	IM0030H23
c 960	10	7.2	26	28	AZ314210	IM0030H23
c 961	10	7.2	26	28	AZ319791	IM0039I05
c 962	10	7.2	26	28	AZ315831	IM0059A11
c 963	10	7.2	26	28	AZ369592	IM0120E16
c 964	10	7.2	26	28	AZ376102	IM0129M14
c 965	10	7.2	26	28	AZ405428	IM0174D13
c 966	10	7.2	26	28	AZ405428	IM0269F08
c 967	10	7.2	26	28	AZ426230	IM0285K16
c 968	10	7.2	26	28	AZ470860	IM0285K16
c 969	10	7.2	26	28	AZ494322	IM0328Q05
c 970	10	7.2	26	28	AZ494322	IM0328Q05
c 971	10	7.2	26	28	AZ641136	IM0571L08
c 972	10	7.2	26	28	AZ769973	IM0571L08
c 973	10	7.2	26	28	AZ780163	IM0571L08
c 974	10	7.2	26	28	AZ795959	IM0571L08
c 975	10	7.2	26	28	AZ818942	IM0571L08
c 976	10	7.2	26	28	AZ856020	IM0160J17
c 977	10	7.2	26	28	AZ938986	IM0160J17
c 978	10	7.2	26	28	AZ938986	IM0160J17
c 979	10	7.2	26	28	AZ953890	IM0219Q15
c 980	10	7.2	26	28	AZ953890	IM0219Q15
c 981	10	7.2	26	28	AZ955924	IM0222P10
c 982	10	7.2	26	28	AZ955924	IM0222P10
c 983	10	7.2	26	28	BH756958	SALK_0549
c 984	10	7.2	26	28	AU258376	AU258376
c 985	10	7.2	26	28	AW327992	dr03d09.x
c 986	10	7.2	26	28	BP979443	602288282
c 987	10	7.2	26	28	BM398876	5009-0-50
c 988	10	7.2	26	28	AZ330939	IM0056E11
c 989	10	7.2	26	28	AZ330939	IM0056E11
c 990	10	7.2	26	28	AZ380695	IM0136E13
c 991	10	7.2	26	28	AZ457313	IM0260P04
c 992	10	7.2	26	28	AZ457313	IM0260P04
c 993	10	7.2	26	28	AZ483323	IM0308J22
c 994	10	7.2	26	28	AZ590063	IM0399M24
c 995	10	7.2	26	28	AZ590063	IM0399M24
c 996	10	7.2	26	28	AZ638891	IM0499I02
c 997	10	7.2	26	28	AZ646274	IM0512P06
c 998	10	7.2	26	28	AZ798068	IM0512P06
c 999	10	7.2	26	28	AZ811377	IM0077B05
c 1000	10	7.2	26	28	AZ811377	IM0077B05

ALIGNMENTS

RESULT 1	AZ609431	28 bp	DNA	linear	GSS 13-DEC-2000
LOCUS	IM0434P17F	Mouse 10kb plasmid	UUGCLM library	Mus musculus, genomic	
DEFINITION	clone UUGCLM0434P17 F, genomic survey sequence.				
ACCESSION	AZ609431				
VERSION	AZ609431.1	GI:11731717			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
	1 (bases 1 to 28)				
	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,				
	Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly				
	, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A.				
	and Wright, D., Weiss, R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb				
JOURNAL	plasmid inserts				
COMMENT	Unpublished				
	Contact: Robert B. Weiss				

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0434 row: P column: 17
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 28.

FEATURES

Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0434P17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed into adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

3 a 7 c 10 g
Query Match 12.4%; Score 17.2; DB 28; Length 28;
Best Local Similarity 86.4%; Pred. No. 4.1e+05;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 20 AGGCAAGCACCAGGCTCAGC 41

Db 28 AGGCAGCAGCCTGGCAGCAGC 7

RESULT 2

LOCUS	AZ330939/c	27 bp	DNA	linear	GSS 29-SEP-2000
DEFINITION	IM0056E11R	Mouse 10kb plasmid	UUGCLM library	Mus musculus genomic	
	clone UUGCLM0056E11 R, genomic survey sequence.				
ACCESSION	AZ330939				
VERSION	AZ330939.1	GI:10393139			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
	1 (bases 1 to 27)				
	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,				
	Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly				
	, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.				
	and Wright, D., Weiss, R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb				
JOURNAL	plasmid inserts				
COMMENT	Unpublished				

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: E column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source

1...27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC1M0056E11"
/sex="Male"

/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 11 a 0 c 12 g 4 t

ORIGIN

Query Match 10.8%; Score 15; DB 28; Length 27;
Best Local Similarity 78.3%; Pred. No. 1.7e+06;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 106 CTCCTCACTCTCCCTATCTTAA 128

Db 26 CTCCTCTCTCTCTCTCTTTAA 4

RESULT 3

AZ861819/c

LOCUS

DEFINITION 2M0168L12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0168L12 R, genomic survey sequence.

ACCESSION AZ861819

VERSION AZ861819.1 GI:13058520

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 24)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Unpublished

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0168 row: L column: 12

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 24.

FEATURES

source

1...24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC2M0168L12"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 9 a 0 c 15 g 0 t

ORIGIN

Query Match 10.5%; Score 14.6; DB 28; Length 24;
Best Local Similarity 81.0%; Pred. No. 2.2e+06;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 106 CTCCTCACTCTCCCTATCTT 126

Db 23 CTCCTCTCTCTCTCTCTCTCT 3

RESULT 4

AZ453525/c

LOCUS

DEFINITION 1M0255A01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0255A01 F, genomic survey sequence.

ACCESSION AZ453525

VERSION AZ453525.1 GI:10611411

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 25)

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL COMMENT

plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0255 row: A column: 01
Seq primer: CGTTGTAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 25.

FEATURES

1. .25
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0255A01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

7 a 9 c 6 g 3 t

Query Match 10.5%; Score 14.6; DB 28; Length 25;
Best Local Similarity 81.0%; Pred. No. 2.2e+06;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 50 TGGTGTCTCTCCAGCGTGT 70
|||||
Db 21 TGGAGTGCCCTCCAGTGTGT 1

RESULT 5
AZ486858/c
LOCUS 28 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0315H19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315H19 R, genomic survey sequence.

ACCESSION AZ486858
VERSION AZ486858.1 GI:10654043
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL COMMENT Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: H column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.

FEATURES

1. .28
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315H19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

6 a 7 c 3 g 12 t

Query Match 10.5%; Score 14.6; DB 28; Length 28;
Best Local Similarity 81.0%; Pred. No. 2.3e+06;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 GCTTGTAGCAGGCGCAAGCA 28
|||||
Db 21 GTTTGTAGGAGAGCAACCA 1

RESULT 6
AZ599021
LOCUS 23 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0414F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0414F08 F, genomic survey sequence.

ACCESSION AZ599021
VERSION AZ599021.1 GI:11721211
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0414 row: F column: 08
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES

source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0414F08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 0 c 15 g 6 t

Query Match 10.1%; Score 14; DB 28; Length 23;
Best Local Similarity 77.3%; Pred. No. 3.2e+06;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 64 GCGTGTGGAGTGGGTTAGG 85
|||||
DB 1 GTGTGTGTAGGTTGGGTTAGG 22
|||||

RESULT 7
AZ309096

LOCUS 26 bp DNA linear GSS 29-SEP-2000
DEFINITION clone UUGC1M0012P15 R, genomic survey sequence.

ACCESSION AZ309096.1 GI:10349744

VERSION GSS.
KEYWORDS Mus musculus (house mouse)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)

REFERENCE
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0012 row: P column: 15
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES

source

1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0012P15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 8 c 6 g 8 t

Query Match 10.1%; Score 14; DB 28; Length 26;
Best Local Similarity 77.3%; Pred. No. 3.3e+06;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 98 GAGATTGGTCCCACTCTCC 119
|||||
DB 4 GAGGCTGGTTACCATCTCTCC 25
|||||

RESULT 8

AAS02482/c

LOCUS

DEFINITION

AA502482
nc71d05.r1 NCI CGAP P1 Homo sapiens CDNA clone IMAGE:772041
similar to SW:RS5_HUMAN P46782 40S RIBOSOMAL PROTEIN S5.; mRNA
sequence.

ACCESSION AA502482

VERSION AA502482.1 GI:2237449

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 28)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL
COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquai, M.D., Michael Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: David B. Krizman, Ph.D.
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 1.

FEATURES

source
 1. 28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:772041"
 /sex="Male"
 /dev_stage="45 years old"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Pri"
 /note="Vector: PAMP10; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into PAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
 6 a 6 c 9 g 7 t

BASE COUNT

ORIGIN
 Query Match 10.1%; Score 14; DB 9; Length 28;
 Best Local Similarity 77.3%; Pred. No. 3.4e+06;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 19 AAGCAAGCAGCAGCTCAG 40
 |||||
Db 27 ATGCCAAGTACTGCTCAG 6

RESULT 9
BH814452
LOCUS
DEFINITION BH814452.1 30 bp DNA linear GSS 02-MAY-2002
 SALK 066400 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_066400, genomic survey sequence.
ACCESSION BH814452
VERSION BH814452.1 GI:20394043
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 30)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

FEATURES

source
 1. 30
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_066400"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
 10 a 1 c 14 g 5 t

BASE COUNT

ORIGIN
 Query Match 10.1%; Score 14; DB 28; Length 30;
 Best Local Similarity 77.3%; Pred. No. 3.5e+06;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 66 GTGCTGGAAGTGGGTAGGAG 87
 |||||
Db 2 GTAGTGTAGAGGATTAGGAG 23

RESULT 10
BZ660808/c
LOCUS
DEFINITION BZ660808.1 26 bp DNA linear GSS 31-JAN-2003
 SALK 024268.26.95-x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_024268.26.95.x, genomic survey sequence.

ACCESSION BZ660808
VERSION BZ660808.1 GI:28173955
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 26)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished
COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At1g55110.

Class: TDNA tagged.

FEATURES

source
 1. 26
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_024268.26.95.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements."

elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

BASE COUNT 9 a 5 c 8 g 4 t
 ORIGIN
 Query Match 9.9%; Score 13.8; DB 29; Length 26;
 Best Local Similarity 88.2%; Pred. No. 3.8e+06;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 55 TCTCTCCAGCGTG 71
 Db 22 TCTCTCCAGCGTG 6

RESULT 11
 AZ818209 27 bp DNA linear GSS 20-FEB-2001
 LOCUS
 DEFINITION 2M0088A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0088A08 F, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 1 (bases 1 to 27)

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
 and Wright, D., Weiss, R.

Mus whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0088 row: A column: 08
 Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends
 High quality sequence stop: 27.

FEATURES
 source

1. .27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clones="UUGC2M0088A08"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number was ligated
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 7 a 6 c 2 g 12 t
 ORIGIN
 Query Match 9.9%; Score 13.8; DB 28; Length 27;
 Best Local Similarity 72.0%; Pred. No. 3.8e+06;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Qy 95 ATGGAGATTGGCTCCCAACTCTCTCC 119
 Db 2 ATAAAATGGTTCTCTACTCTCTCC 26

RESULT 12
 AZ990764

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0274 row: F column: 09

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 28.

FEATURES

source

1. .28

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUGC2M0274F09"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

Mon Aug 25 09:45:55 2003

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into cells chemically-competent E. coli XL10-Gold (Stratagene) and selected for ampicillin resistance."

BASE COUNT 7 a 3 c 9 g 9 t
 ORIGIN
 Query Match 9.9%; Score 13.8; DB 28; Length 28;
 Best Local Similarity 72.0%; Pred. No. 3.9e+06;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 72 GAAGTTGGGCTTAGGAGTACGGAGAT 96
 |||||
 Db 4 GAAGTTGGGCTTGTGAACGTACAT 28

RESULT 13
 AZ317165/c 24 bp DNA linear GSS 29-SEP-2000
 LOCUS
 DEFINITION
 1M0035H03R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGCLM0035H03 R, genomic survey sequence.

ACCESSION
 AZ317165
 VERSION
 AZ317165.1 GI:10365702
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
 1 (bases 1 to 24)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.,
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

UNPUBLISHED
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0035 row: H column: 03
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /mol_type="Genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0035H03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M.
 Laboratory Mouse DNA Resource
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative

FEATURES
 source
 1..24
 /organism="Mus musculus"
 /mol_type="Genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0035H03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M.
 Laboratory Mouse DNA Resource
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into cells
 chemically-competent E. coli XL10-Gold (Stratagene) and
 selected for ampicillin resistance."

BASE COUNT 7 a 8 c 1 g 8 t
 ORIGIN
 Query Match 9.8%; Score 13.6; DB 28; Length 24;
 Best Local Similarity 80.0%; Pred. No. 4.2e+06;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 76 TTGGGTTAGGAGTACGGAGA 95
 |||||
 Db 24 TTGGGTTAGGAGTACGTAAGA 5

RESULT 14
 AA868839 25 bp mRNA linear EST 04-JAN-1999
 LOCUS
 DEFINITION
 ak54904.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1409814
 3' similar to TR:Q14679 Q14679 KIAA0173 PROTEIN. ; mRNA sequence.

ACCESSION
 AA868839
 VERSION
 AA868839.1 GI:2964284
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 1 (bases 1 to 25)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

UNPUBLISHED
 Contact: Robert Strausberg, Ph.D.
 Email: cga@nci.nih.gov
 CNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
 , Ph.D.
 CNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LEML at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Insert Length: 1057 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1409814"
 /sex="male"
 /lab_host="DH10B"
 /clone_lib="Soares testis NHT"
 /notes="Vector: pT73-Pac (Pharmacia) with a modified
 polylinker; Site: 1: Not 1; Site 2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from clontech Laboratories
 , Inc., and primed with a Not I - oligo(dT) primer [5',
 TGTTACCATCTGAGTGGCGCCGCCAATTTTTCCTTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia) digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization to Cot5, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 5 a 8 c 6 g 6 t
 ORIGIN

	Query Match	9.8%	Score 13.6	DB 9	Length 25
	Best Local Similarity	80.0%	Pred. NO. 4.2e+06		
	Matches .16	Conservative 0	Mismatches 4	Indels 0	Gaps 0
dy	34	CTCACAGCTGGAAACCCCTGGT	53		
db	1	CTCCCATGTGGAAACCCCTTGT	20		

RESULT 15	linear	DNA	GSS 29-SEP-2000
AZ303426/c	27 bp		
LOCUS			
DEFINITION	Mouse 10kb plasmid UUGCIM library Mus musculus genomic		
clone	UUGCIM0003A09 F, genomic survey sequence.		
ACCESSION	AZ303426		
VERSION	AZ303426.1	GI:10338804	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 27) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
UNPUBLISHED			
CONTACT: Robert B. Weiss			
COMMENT			

UT
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: A column: 09
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 27.

BASE COUNT
ORIGIN

3 a 8 c 7 g

1. .27
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0003A09"
/sex="Male"
/lab_hosts="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gl14732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	9.8%;	Score 13.6;	DB 28;	Length 27;
Best Local Similarity	80.0%;	Pred. No. 4.4e+06;		
Matches	16;	Conservative	0;	Mismatches 4;
				Indels 0;
2y	28	ACCAGGCTCACAGCTGGAAC	47	
db	23	ATCAGGCTCACAGGTAGGAC	4	
RESULT 16				
AI635476/c	28 bp	mrna	linear	EST 26-APR-1999
LOCUS	AI635476			
DEFINITION	t865903.x1 NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:223468 3;			
	similar to TR:Q62107 Q62107 PROLINE-RICH SALIVARY PROTEIN ; contains			
	MRP22 b1 MGR1 repetitive element ; mRNA sequence.			

RESULT 16	
AI635476/c	
LOCUS	linear
DEFINITION	28 bp mRNA EST 26-APR-1999
	c65503.x1 NCI CGAP Kids Homo sapiens CDNA clone IMAGE:2233468 3,
	similar to TR_062107 Q62107 PROLINE-RICH SALIVARY PROTEIN ; contains
	MER22.B1 MSRI repetitive element ;, mRNA sequence.
ACCESSION	AI635476
VERSION	AI635476
KEYWORDS	EST.
SOURCE	AI635476.1 GI:4586806
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 28)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL	Tumor Gene Index
COMMENT	Unpublished
	Contact: Robert Strausberg, Ph.D.

Email: cgapbs@email.nih.gov
Tissue Procurement: Christoffer Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/abbr/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES	source	Location/Qualifiers
1..28		
/organism="Homo sapiens"		
/mol_type="rRNA"		
/db_xref="taxon:9606"		
/clone="IMAGE:2233468"		
/tissue_type="renal cell tumor"		
/lab_host="DH10B"		
/clone_lib="NCI CGAP Kid8"		
/note="Organ: Kidney; Vector: pSite 2; NotI; Cloned unidirectional. Average insert size 1.2 kb. Lif		
11524-014"		
6	14 C	8 g 0 t
BASE COUNT		

Query Match 9.8%; Score 13.6; DB 9; Length 28;
Best Local Similarity 67.9%; Pred. No. 4.4e+06;
Matches 19: Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY
58 CCTCCAGCGTGGTGGAAGTTGGGTAGG 85

DH
28 CCCC CGGGGGTGGTGGTCGCTGGG 1

RESULT 17	
BH810072/c	
LOCUS	BH810072
DEFINITION	SALK_040645 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_040645, genomic survey sequence.
ACCESSION	BH810072

VERSION BH810072.1 GI:20387889
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Arabidopsi
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 , C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
 , Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 JOURNAL Arabidopsis Genome
 COMMENT Unpublished
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At3g32895.
 Class: TDNA tagged.

FEATURES

source
 1..28
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_040645"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /notes="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 7 a 9 c 4 g 8 t
 ORIGIN

Query Match 9.8%; Score 13.6; DB 28; Length 28;
 Best Local Similarity 80.0%; Pred. No. 4.4e+06;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 GCTTGTAGCAGAGGCAAGC 27

Db 27 GCTTGTAGCTGAGGAAAGC 8

RESULT 18
 BH810091/c
 LOCUS BH810091 28 bp DNA linear GSS 02-MAY-2002
 DEFINITION SALK_040694 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_040694, genomic survey sequence.

ACCESSION BH810091

VERSION BH810091.1 GI:20387908

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids II; Brassicales; Brassicaceae; Arabidopsi
 REFERENCE 1 (bases 1 to 28)

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
 , C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
 , Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 JOURNAL Arabidopsis Genome
 COMMENT Unpublished

Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At3g32895.
 Class: TDNA tagged.

FEATURES

source
 1..28
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_040694"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /notes="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 7 a 9 c 4 g 8 t
 ORIGIN

Query Match 9.8%; Score 13.6; DB 28; Length 28;
 Best Local Similarity 80.0%; Pred. No. 4.4e+06;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 GCTTGTAGCAGAGGCAAGC 27

Db 27 GCTTGTAGCTGAGGAAAGC 8

RESULT 19

BH810140/c

LOCUS BH810140 28 bp DNA linear GSS 02-MAY-2002

DEFINITION SALK_041353 Arabidopsis thaliana TDNA insertion lines Arabidopsis

thaliana genomic clone SALK_041353, genomic survey sequence.

ACCESSION BH810140

VERSION BH810140.1 GI:20387958

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE 1 (bases 1 to 28)

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

, C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

, Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL Arabidopsis Genome

COMMENT Unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At3g32895.

Class: TDNA tagged.

FEATURES

source

1..28

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_041353"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

```

BASE COUNT      7 a      9 c      4 g      8 t
ORIGIN
Query Match      9.8%; Score 13.6; DB 28; Length 28;
Best Local Similarity 80.0%; Pred. No. 4.4e+06;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 GCTTGTAGCAGGACGAC 27
    |||||
Db 27 GCTTGTAGCTGAGGAAAGC 8

```

```

RESULT 20
AZ481978      27 bp      DNA      linear      GSS 04-OCT-2000
LOCUS      1M0306K11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0306K11 R, genomic survey sequence.
ACCESSION      AZ481978.1 GI:10643043
VERSION
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0306 row: K column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0306K11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

```

```

FEATURES
source
1..27
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0306K11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

```

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

BASE COUNT      3 a      13 c      5 g      6 t
ORIGIN
Query Match      9.6%; Score 13.4; DB 28; Length 27;
Best Local Similarity 73.9%; Pred. No. 5e+06;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 105 GCTCCCACTCTCTCTATCTTA 127
    |||||
Db 5 GGTCCCCACTCTCTGTACCCCA 27

```

```

RESULT 21
BE389833/c
LOCUS      601284336F1 NTH_MGC_44 Homo sapiens cDNA clone IMAGE:3606177 5',
DEFINITION      mRNA sequence.
ACCESSION      BE389833
VERSION      BE389833.1 GI:9335198
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
1 (bases 1 to 30)
NIH-MGC http://mgs.nci.nih.gov/
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM255 row: 9 column: 10
High quality sequence start: 10
High quality sequence stop: 28.
Location/Qualifiers
1..30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="NIH MGC 44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

```

```

FEATURES
source
1..30
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="NIH MGC 44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

```

```

BASE COUNT      7 a      4 c      12 g      7 t
ORIGIN
Query Match      9.6%; Score 13.4; DB 10; Length 30;
Best Local Similarity 73.9%; Pred. No. 5.2e+06;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 108 CCCAATCTCTCTATCTTAAG 130
    |||||
Db 26 CCAGCCTCGTACCTAGCTAAAG 4

```

```

RESULT 22
AZ474193
LOCUS
DEFINITION
  AZ474193 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0290J02 R, genomic survey sequence.
ACCESSION
  AZ474193
VERSION
  AZ474193.1 GI:10632318
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 30)
REFERENCE
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
  M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
  and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished
JOURNAL
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0290 row: J column: 02
  Seq primer: CACACAGGAAACACGTATGACC
  Class: plasmid ends
  High quality sequence stop: 30.
FEATURES
  source
  1..30
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC1M0290J02"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC1M library"
  /note="Vector: PWD42nv; Purified genomic DNA from M.
  musculus C57BL/6J (male) was obtained from the Jackson
  Laboratory Mouse DNA Resource
  (http://www.jax.org/resources/documents/dnares/). The DNA
  was hydrodynamically sheared by repeated passage through a
  0.005 inch orifice at constant velocity. The sheared DNA
  was blunt end-repaired with T4 DNA polymerase and T4
  polynucleotide kinase. Adaptor oligonucleotides were
  ligated to the blunt ends in high molar excess. The
  adaptor DNA was purified and size-selected for a 9.5 to
  10.5 kb range using preparative agarose gel
  electrophoresis. Vector DNA was prepared from a derivative
  of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
  inducible derivative of plasmid R1. The vector was ligated
  with adaptors complementary to the insert adaptors and
  purified. The sheared, adaptor mouse DNA was annealed to
  adaptor vector DNA, and transformed into
  chemically-competent E. coli XL10-Gold (Stratagene) cells
  and selected for ampicillin resistance."
  8 a 8 c 10 g 4 t
BASE COUNT
  8 a 8 c 10 g 4 t
ORIGIN
  Query Match 9.6%; Score 13.4; DB 28; Length 30;
  Best Local Similarity 73.9%; Pred. No. 5.2e+06;
  Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

  QY 26 GCACCGAGCTACACGTGGAC 48
  Db 8 GCACAGACACACACGTGGAC 30
  COMMENT
  26 GCACCGAGCTACACGTGGAC 48
  8 GCACAGACACACACGTGGAC 30

```

```

RESULT 23
AB082245
LOCUS
DEFINITION
  AB082245 Drosophila melanogaster DNA, clone:1(2)SH2 0721, genomic survey
  sequence.
ACCESSION
  AB082245
VERSION
  AB082245.1 GI:23307282
KEYWORDS
  GSS.
SOURCE
  Drosophila melanogaster (fruit fly)
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
  1
REFERENCE
  Oh, S.W., Kingsley, T., Shin, H.H., Zheng, Z., Chen, H.W., Chen, X.,
  Wang, H., Ruan, P., Moody, M. and Hou, S.X.
  A p-element insertion screen identified mutations in 455 novel
  essential genes in Drosophila
  Genetics 163 (1), 195-201 (2003)
  22474228
  12586707
REFERENCE
  2 (bases 1 to 30)
  Direct Submission
  Submitted (24-MAR-2002) Suwan Oh, The Laboratory of Immunobiology,
  National Institutes of Health, National Cancer Institute,
  Frederick; 1050 Boyles st., Frederick, Maryland 21702-1201, USA
  (E-mail:ohsuwan@mail.ncifcrf.gov, Tel:1-301-846-7314,
  Fax:1-301-846-6145)
FEATURES
  source
  1..30
  /organism="Drosophila melanogaster"
  /mol_type="genomic DNA"
  /db_xref="taxon:7227"
  /clone="1(2)SH2 0721"
  7 a 6 c 12 g 5 t
BASE COUNT
  7 a 6 c 12 g 5 t
ORIGIN
  Query Match 9.6%; Score 13.4; DB 29; Length 30;
  Best Local Similarity 73.9%; Pred. No. 5.2e+06;
  Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

  QY 6 GGCTTGTAGCAGACGACGCA 28
  Db 4 GGCCGGTAACAGAGCGGTCA 26

RESULT 24
TAI79D12P/c
LOCUS
DEFINITION
  TAI79D12P T. brucei sheared genomic DNA clone 179d12, forward sequence,
  genomic survey sequence.
ACCESSION
  AL474655
VERSION
  AL474655.1 GI:11839841
KEYWORDS
  GSS.
SOURCE
  Trypanosoma brucei
  Trypanosoma brucei
  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
  Trypanosoma.
  1 (bases 1 to 30)
REFERENCE
  Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
  Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
  Melville, S.B., Rajadream, M.A. and Barrell, B.G.
  Direct Submission
  Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
  project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
  Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
  nh@sanger.ac.uk
  Constructed at the Institute for Genomic Research (TIGR),
  Rockville, MD. Genomic DNA isolated from a cloned population of
  Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
  to give a tight size distribution (

```

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: neleaved@igr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1..30
Location/Qualifiers
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="179d12"

BASE COUNT 10 a 7 c 6 g 7 t
ORIGIN

Query Match 9.6%; Score 13.4; DB 29; Length 30;
Best Local Similarity 73.9%; Pred. No. 5.2e+06;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 60 TCCAGCGTGGTGGAGTTGGGTT 82
||||| ||||| ||||| |||||
DB 30 TCCACCGTCGTAGAAATGTGTT 8

RESULT 25

AZ421118/c
LOCUS AZ421118 21 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0199D16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0199D16 F, genomic survey sequence.

ACCESSION AZ421118
VERSION AZ421118.1 GI:10545131
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0199 row: D column: 16
Seq primer: CCGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source
1..21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0199D16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource"

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 8 c 7 g 4 t
ORIGIN

Query Match 9.5%; Score 13.2; DB 28; Length 21;
Best Local Similarity 83.3%; Pred. No. 5.2e+06;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 31 AGGCTCACAGCTGGACCC 48
||||| ||||| ||||| |||||
DB 21 AGGCTCACAGCTGGACCC 4

Search completed: August 22, 2003, 11:04:43
Job time : 1699 secs